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OM nucleic - nucleic search, using sw model

Run on: November 22, 2000, 00:37:25 ; Search time 1014.24 Seconds
(without alignments)
3608.645 Million cell updates/sec

Title: US-08-955-572-1
Perfect score: 838
Sequence: 1 aatcagcttcttagtatca.....aatagggtgtgggacttt 838

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues
Total number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl :
1: gb_ba1 :
2: gb_ba2 :
3: gb_om :
4: gb_ov :
5: gb_pat :
6: gb_ph :
7: gb_pl1 :
8: gb_pl2 :
9: gb_pr1 :
10: gb_pr2 :
11: gb_pr3 :
12: gb_ro :
13: gb_sy :
14: gb_un :
15: em_fun :
16: em_hum1 :
17: em_hum2 :
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21: em_ov :
22: em_pat :
23: em_ph :
24: em_pl :
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26: em_sts :
27: em_sy :
28: em_un :
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32: gb_in2 :
33: gb_in3 :
34: gb_pl3 :
35: gb_pr4 :
36: em_ba1 :
37: em_ba2 :
38: em_htg1 :
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42: em_htg5 :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	836.4	99.8	1415	5 I68025	I68025 Sequence 7
2	836.4	99.8	1415	66 HS003397	U03397 Human recep
3	836.4	99.8	1415	91 G28572	G28572 human STS S
4	833.2	99.4	1419	67 HUMILAX	L12964 Human activ
5	339.2	40.5	2350	12 MUSTC41BB	J04492 Mouse T-cel
6	331.4	39.5	768	5 I68024	I68024 Sequence 5
c 7	144.8	17.3	65848	65 HS892F13	AL009183 Human DNA
8	144.8	17.3	162975	78 AC025225	AC025225 Homo sapi
c 9	144.8	17.3	202773	78 AC025220	AC025220 Homo sapi
10	138	16.5	183911	88 AL365441	AL365441 Homo sapi
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13 72.2 8.6 12260 12 MMU02567
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18 38.2 4.6 156399 9 AC002456
19 37 4.4 92128 8 F1707
20 37 4.4 146863 84 AC073392
21 37 4.4 195577 86 AL139816
22 36.8 4.4 12460 12 RNO010709
23 36.8 4.4 179381 81 AC055863
24 36.6 4.4 114771 65 HS569D19
25 36.4 4.3 11172 71 AC013030
26 36.4 4.3 56820 33 DMBR7C10
27 36.4 4.3 94585 66 HSDJ401P4
28 36.4 4.3 289090 31 AED03424
29 36.2 4.3 174128 89 AP001123
30 36.2 4.3 196292 84 AC073388
31 36 4.3 1784 66 HSFAAH03
32 36 4.3 122865 85 AL137799
33 36 4.3 126613 66 HSJ603114
34 36 4.3 129536 90 HSDJ8L15
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36 36 4.3 194399 86 AL157894
37 35.8 4.3 3133 5 I15000
38 35.8 4.3 3135 4 GCCEK6A
39 35.8 4.3 86224 88 AL360174
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43 35.4 4.2 179651 9 AC005553
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45 35.2 4.2 153863 78 AC025361

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ALIGNMENTS

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RESULT 1
168025 LOCUS I68025 1415 bp DNA PAT 04-FEB-1998
DEFINITION Sequence 7 from patent US 5674704.
ACCESSION I68025
VERSION I68025.1 GI:2830147
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1415)
AUTHORS Goodwin,R.G., Smith,C.A. and Alderson,M.R.
TITLE Cytokine designated 4-TBB ligand
JOURNAL Patent: US 5674704-A 7 Oct-1997;
FEATURES Location/Qualifiers
source 1. 1415
BASE COUNT 385 a 332 c 333 g 365 t
ORIGIN
Query Match 99.8%; Score 836.4; DB 5; Length 1415;
Best Local Similarity 99.9%; Pred. No. 1.le-245;
Matches 837; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 aatcagctttagtatacatatcattgtccagatttcacatgggaacagctgttaca 60
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Db 80 AATCAGCTTTGCTAGTATCATACCTGTGCCAGATTTCATGCGAAGAACAGCTGTACAA 139
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Qy 61 catagtagcactctgttgcctcaactttgagaggacaagatcattgcagatcc 120
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Qy 121 ttgtagtaactgcccagctggtacattctgtgataataacaggaatcagattgcagtc 180
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Qy 361 acaaggtcaagaactgacaaaaaagggtgttaaaactgttcttgggacatttaacga 420
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Db 680 CATCTCCCTCTTCTTGTGCGCTGACGTGCGTGTCTCTCTCTCTCTCTCTCTCTAC 739
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Db 800 ATTTATGAGACCAAGTACAACTACTCAAGAGGAAGATGGCTAGCTGCGGATTTCCAGA 859
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DEFINITION Human receptor protein 4-1BB mRNA, complete cds.
ACCESSION U03397
VERSION U03397.1 GI:571320
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1415)
AUTHORS Alderson,M.R., Smith,C.A., Tough,T.W., Davis-Smith,T.,
Armstrong,R.J., Falk,B., Roux,E., Baker,E., Sutherland,G.R.,
Din,W.S. and Goodwin,R.G.
Molecular and biological characterization of human 4-1BB and its
ligand
JOURNAL Eur. J. Immunol. 24 (9), 2219-2227 (1994)
MEDLINE 94374434
REFERENCE 2 (bases 1 to 1415)
AUTHORS Alderson,M.
TITLE Direct Submission
JOURNAL Submitted (10-NOV-1993) Mark Alderson, Immunex Research and
Development Corp., 51 University St., Seattle, WA 98101, USA
FEATURES Location/Qualifiers
source 1. .1415

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385 a 332 c 333 g 365 t
BASE COUNT
ORIGIN

Query Match 99.8%; Score 836.4; DB 66; Length 1415;
Best Local Similarity 99.9%; Pred. No. 1.1e-245;
Matches 837; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 aatcagcttgtagtatcatatcctgagccagatttcattcatatggaagacagctgttacaa 60
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DB 80 AATCAGCTTGTGCTAGTATCATCTGTGCCAGATTTCATCATGTGGGAACAGCTGTTCACAA 139
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QY 61 catagtagccactctgttgcgtgcctcaactttgagagagacagatcattgcaggatcc 120
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DB 140 CATAGTAGCCACATCTGTTGCTGCTCAACTTTGAGAGGACAAAGATCATTCAGGATCC 199
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QY 121 ttgtagtaactgccagctggtgacattctctgtgataataacagagaatcagatttcagctcc 180
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DB 200 TTGTAGTAAGTGCACAGCTGGTGTGATTAATACAGGAATCAGATTTGCAGTCC 259
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QY 181 ctgtctccaaatagtttctccagccagctggacaaagacctgtgacatatgcaggca 240
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DB 260 CTGTCTCCAAATAGTTTCTCCAGCCAGGTGGACAAAGACCTGTGACATATGCAGGCA 319
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DB 380 CTGCACTCCAGGGTTTCACTGCCTGGGGCAGGATGCAGCATGTGTGAACAGGATTGTAA 439
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QY 361 acaaggtcaagaactgacaaaaaaggttgtaaagactgtgtcttgggacatttaacga 420
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DB 440 ACAAGGTCAAGAACTGACAAAAGAGTGTGAAGACTGTGTCTTGGGACATTTAAACGA 499
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QY 781 agaagaagaaggaggtgtgaaactgtgaaatggaagtcaatagggctgttgggacttt 838
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Db 860 AGAAGAAGAAGGAGGATGTAACGTGAAATGGAAGTCAATAGGCTGTTGGGACTTT 917
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RESULT 3
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LOCUS human STS SHGC-35316, sequence tagged site. STS
DEFINITION G28572
ACCESSION G28572
VERSION G28572.1 GI:1408387
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1415)
AUTHORS Myers,R.M.
JOURNAL Unpublished (1996)
COMMENT
Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu
Primer A: TGAATGGAGTCAATATGAGG
Primer B: AAAAAGTGGTCAATTTTAAAGG
STS size: 180
PCR Profile:
Initial incubation: 94 degrees C for 90 seconds
Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600
Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/ul
Total Vol: 10 ul
Buffer:
MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

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Prepared with primer pairs provided by Sandoz, derived from U03397
 -- Washington University/Merck EST sequence.

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QY 241 ggtataagtggttttcagagaccagaagagtggttctccaccagacaatgcagagtgtga 300
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QY 421 tcagaaactggcatctgtcgaccttgacaaacttcttcttgatggaaagctgtgct 480
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Db 820 ATTTATGAGACCAGTACAAACTACTCAAGAGGAAGATGCTGTAGCTGCCGATTTCCAGA 879
QY 781 agaagaagaagagagtgtaactgtgaatggaaatgaatagggtgttggacttt 838
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RESULT 5
MUSC41BB 2350 bp mRNA ROD 27-APR-1993
LOCUS Mouse T-cell receptor 4-1BB protein mRNA, complete cds.
DEFINITION
ACCESSION J04492
VERSION J04492.1 GI:201121
KEYWORDS T-cell receptor
SOURCE Mouse (strain C57BL/6) T-lymphocyte cell lines L2 and L3, cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Kwon,B.S. and Weissman,S.M.
TITLE cDNA sequences of two inducible T-cell genes
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967 (1989)
MEDLINE 8918457
COMMENT Draft entry and clean copy of sequence for [1] kindly provided by B.S.Kwon, 17-MAR-1989.
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ORIGIN Unreported.

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Matches 537; Conservative 0; Mismatches 243; Indels 12; Gaps 4;

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RESULT	6
I68024	
LOCUS	I68024 768 bp DNA PAT 04-FEB-1998
DEFINITION	Sequence 5 from patent US 5674704.
ACCESSION	I68024
VERSION	I68024.1 GI:2830146
KEYWORDS	.
SOURCE	Unknown..
ORGANISM	Unknown..
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 768)
TITLE	Goodwin,R.G., Smith,C.A. and Alderson,M.R.
JOURNAL	Cytokine designated 4-TBB ligand
FEATURES	Patent: US 5674704-A 5 07-OCT-1997;
	Location/Qualifiers
	1..768
source	/organism="unknown"
- BASE COUNT	188 a 186 c 217 g 177 t
- ORIGIN	
	Query Match 39.5%; Score 331.4; DB 5; Length 768;
	Best Local Similarity 68.2%; Pred. No. 1.3e-90;
	Matches 522; Conservative 0; Mismatches 231; Indels 12; Gaps 4;
QY	41 atgggaacagcgtgttacaaatagtagcacctctgtgcttggttgcctcaactttgagagg 100
Db	1 ATGGGAACAACATGTTTACAAACGTGGTGTCATTGTGCTGCTAGTGGCGTGTGAGAAG 60
QY	101 acaaagtattcgagatccttgttagtaactcccagctggttacattctgtgataataac 160
Db	61 GTGGGAGCCGTGCAGAACTCCTGTGATAACTGTCACTCTGGCTGGTACTTCTTCGAAAAAATAC 120
QY	161 aggaatcagaattgcagtcctctccatcaaatagtttctccagcgcaggtggacaagg 220
Db	121 ---AATCCAGTCTCGAAGAGCTGCCCTCCAAGTACTTCTCCAGCATAGGTGGACAGCG 177
QY	221 acctgtgacatatgcaggcagtgtaaagggtgtttcaggaccaggagaagtggtccctcc 280
Db	178 AACTGTAAATCTGCAAGATGTGTGCAGCTATTTTCAGGTTCAAAGAAGTTTGTCTCCTCT 237
QY	281 accagaatgcagagtgtagtcacctccaggtttcactgctcctggggcaggatgcagc 340
Db	238 ACCCACAAACGGGAGTGTGAGTGCATTGAAGAGATTCCATTGCTTGGGCCACAGTGCACC 297
QY	341 atgtgtgaacagattgttaacaaaggtcaagaactgacaaaaaaaaggttctaagaactgt 400
Db	298 AGATGTGAAGAGACTGCAGGCCTGGCCAGGAGCTAACGAAGCAGGTTTGCAAAAACCTGT 357
QY	401 tgctttggagacatttaacgatcagaaacg---tgccatctgtcgaccttgagacaactgt 457
Db	358 AGCTTGGGAACAATTAATGACCAGAACGGTACTGGCGTCTGTFCGACCTTGGACGAACATGC 417
QY	458 tccttggatgaaagtctgtgcttggatggagcgaagagagacgtggtctgtgga 517
Db	418 TCTCTAGCGGAAGTCTGTGCTTAAGACCGGAGCACCGAAGAAAGACGTGGTGTGTGGA 477
QY	518 ccattctccagctgacctctctccggagagcatcctctgtgacccccgccctgcctcgcgaga 577
Db	478 CCCCCTGTGTGAGCTTCTCTCCAG---TACCACCATTTCTGTGACTCCAGAGGGAGGA 534
QY	578 gagcaggacacatctccgagatcatcctctcttttttctgtgctgacgtcgactcggttg 637
Db	535 CCAGGAGGACATCTCTTGACAGTCTTACCTTGTTCCTGGCGCTGACATCG---GCTTTG 591
QY	638 ctcttctcctgttcttctcacgtccgtttctctctgtttaaaccggggcagaagaaga 697
Db	592 CTGCTGCCCTGATCTTCATTACTCTCCTGTCTCTGTGCTCAATGGATCAGGAAAAA 651
QY	698 ctctgttatattcaaacacacatttatagaccagtcacaactactcaagaggagaat 757
Db	652 TTCCCCCAGATATTCAAGCAACCATTTTAAGAGAGACCATCTGGAGCAGCTCAAGAGGAAGAT 711

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repeat_region /note="MIR repeat: matches 28. .218 of consensus"
repeat_region 3734. .4064
repeat_region /note="AluX repeat: matches 1. .312 of consensus"
repeat_region 4115. .4375
repeat_region /note="AluX repeat: matches 1. .245 of consensus"
repeat_region 4377. .4668
repeat_region /note="AluY repeat: matches 1. .291 of consensus"
repeat_region 4669. .4733
repeat_region /note="AluX repeat: matches 232. .296 of consensus"
repeat_region 5240. .5454
repeat_region /note="AluDb repeat: matches 39. .299 of consensus"
repeat_region 5455. .5888
repeat_region /note="L1M8 repeat: matches 5622. .6097 of consensus"
repeat_region 5889. .6147
repeat_region /note="AluX repeat: matches 54. .312 of consensus"
repeat_region 6148. .6355
repeat_region /note="L1M8 repeat: matches 6097. .6289 of consensus"
repeat_region 6365. .6579
repeat_region /note="L1M2 repeat: matches 5869. .6086 of consensus"
repeat_region 6749. .7061
repeat_region /note="MLT1D repeat: matches 197. .505 of consensus"
repeat_region 7062. .7378
repeat_region /note="AluX repeat: matches 1. .306 of consensus"
repeat_region 7379. .7570
repeat_region /note="MLT1D repeat: matches 5. .197 of consensus"
repeat_region 7625. .7688
repeat_region /note="L2 repeat: matches 2638. .2709 of consensus"
repeat_region 7823. .8112
repeat_region /note="AluDb repeat: matches 1. .311 of consensus"
repeat_region 8714. .8755
repeat_region /note="21 copies 2 mer tt 76% conserved"
repeat_region 8766. .9065
repeat_region /note="AluDb repeat: matches 1. .309 of consensus"
repeat_region 9188. .9257
repeat_region /note="MERA repeat: matches 10. .79 of consensus"
repeat_region 9292. .9530
repeat_region /note="AluSg repeat: matches 1. .290 of consensus"
repeat_region 9679. .9986
repeat_region /note="AluSg repeat: matches 1. .308 of consensus"
repeat_region 10829. .10912
repeat_region /note="L1 repeat: matches 4918. .5003 of consensus"
repeat_region 10933. .10989
repeat_region /note="L1 repeat: matches 3505. .3562 of consensus"
repeat_region 11295. .11589
repeat_region /note="AluSg repeat: matches 1. .291 of consensus"
repeat_region 11793. .12183
repeat_region /note="L1M4 repeat: matches 4475. .4848 of consensus"
repeat_region 12184. .12478
repeat_region /note="AluSg repeat: matches 1. .292 of consensus"
repeat_region 12479. .12806
repeat_region /note="L1M4 repeat: matches 4099. .4475 of consensus"
repeat_region 12808. .13063
repeat_region /note="LTR42 repeat: matches 252. .495 of consensus"
repeat_region 13064. .13333
repeat_region /note="AluY repeat: matches 36. .303 of consensus"
repeat_region 13334. .13478
repeat_region /note="LTR42 repeat: matches 66. .252 of consensus"
repeat_region 13479. .13851
repeat_region /note="MSTB repeat: matches 1. .426 of consensus"
repeat_region 13852. .13921
repeat_region /note="LTR42 repeat: matches 1. .66 of consensus"
repeat_region 13922. .14007
repeat_region /note="L1M4 repeat: matches 4017. .4102 of consensus"
repeat_region 14105. .14264
repeat_region /note="AluJ repeat: matches 136. .294 of consensus"
repeat_region 14314. .14507
repeat_region /note="MLT1P repeat: matches 314. .520 of consensus"
misc_feature complement(14508. .14664)
repeat_region /note="match: STS: Em:AL034007"
repeat_region 14707. .15011
repeat_region /note="AluDb repeat: matches 1. .305 of consensus"
repeat_region 15087. .15385
repeat_region /note="AluX repeat: matches 1. .295 of consensus"
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repeat_region 15407. .15757
repeat_region /note="L1M4 repeat: matches 3340. .3690 of consensus"
repeat_region 15781. .16029
repeat_region /note="L2 repeat: matches 1847. .2113 of consensus"
repeat_region 16060. .16113
repeat_region /note="MIR repeat: matches 196. .250 of consensus"
repeat_region 16126. .16159
repeat_region /note="17 copies 2 mer ta 82% conserved"
repeat_region 16167. .16222
repeat_region /note="28 copies 2 mer tg 71% conserved"
repeat_region 16225. .16310
repeat_region /note="MIR repeat: matches 120. .204 of consensus"
repeat_region 16382. .16481
repeat_region /note="L2 repeat: matches 1694. .1797 of consensus"
repeat_region 16466. .16621
repeat_region /note="L2 repeat: matches 2260. .2417 of consensus"
repeat_region 17192. .17311
repeat_region /note="AluJ repeat: matches 2. .126 of consensus"
repeat_region 17580. .17953
repeat_region /note="187 copies 2 mer cc 60% conserved"
repeat_region 17625. .17954
repeat_region /note="110 copies 3 mer cct 78% conserved"
repeat_region 17986. .18280
repeat_region /note="AluSg repeat: matches 1. .293 of consensus"
repeat_region 18808. .19092
repeat_region /note="AluJo repeat: matches 34. .306 of consensus"
repeat_region 19215. .19517
repeat_region /note="AluX repeat: matches 1. .304 of consensus"
repeat_region 19617. .19728
repeat_region /note="MLT2FB repeat: matches 1. .119 of consensus"
repeat_region 19729. .20034
repeat_region /note="AluSp repeat: matches 1. .308 of consensus"
repeat_region 20035. .20048
repeat_region /note="MLT2FB repeat: matches 119. .132 of consensus"
repeat_region 20049. .20127
repeat_region /note="MADE1 repeat: matches 1. .80 of consensus"
repeat_region 20128. .20297
repeat_region /note="MLT2FB repeat: matches 132. .279 of consensus"
misc_feature complement(20298. .20609)
misc_feature /note="match: GSS: Em:AQ425759"
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repeat_region /note="match: GSS: Em:B75776"
repeat_region 20993. .21102
repeat_region /note="55 copies 2 mer aa 75% conserved"
repeat_region 21561. .21859
repeat_region /note="AluX repeat: matches 1. .299 of consensus"
repeat_region 21958. .22249
repeat_region /note="AluJo repeat: matches 2. .299 of consensus"
repeat_region 22472. .22611
repeat_region /note="AluSg repeat: matches 1. .142 of consensus"
repeat_region 22612. .22907
repeat_region /note="AluX repeat: matches 1. .301 of consensus"
repeat_region 22908. .23072
repeat_region /note="AluSg repeat: matches 142. .300 of consensus"
repeat_region 23255. .23400
repeat_region /note="THE1B repeat: matches 219. .364 of consensus"
repeat_region 23401. .23682
repeat_region /note="AluSc repeat: matches 1. .295 of consensus"
repeat_region 23683. .23823
repeat_region /note="THE1B repeat: matches 1. .220 of consensus"
repeat_region 23868. .24164
repeat_region /note="AluX repeat: matches 14. .308 of consensus"
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Query Match 17.3%; Score 144.8; DB 65; Length 65848;
Best Local Similarity 95.5%; Pred. No. 5.6e-33;
Matches 149; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 233 tgcaggcagtgttaaagggttttcaggaccaggaaaggagtgttcctccaccaccaatgca 292
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 52938 TGGGGGACTTTGTAGTGTGTTTCAGGACGAGGAAGAGTGTTCCTCCACCAATGCA 52879

QY 293 gagtgtgactgcactccagggtttcactgcctgtggggcaggatgcagcatgtgtgaacag 352
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
```


Contact: humquery@sanger.ac.uk
 ----- Project Information
 Center project name: ba417D2
 ----- Summary Statistics
 Assembly program: XGAP4; version 4.5
 Sequencing vector: M13; M7815; 21% of reads
 Sequencing vector: plasmid; L08752; 78% of reads
 Chemistry: Dye-terminator ABI; 33% of reads
 Chemistry: Dye-terminator Big Dye; 56% of reads
 Chemistry: Dye-terminator-amersham; 8% of reads
 Chemistry: Dye-terminator Big Dye; 1% of reads
 Consensus quality: 180899 bases at least Q40
 Consensus quality: 181444 bases at least Q30
 Consensus quality: 181859 bases at least Q20
 Insert size: 182911; sum-of-contigs
 Insert size: 176659; 3.8% error; agarose-fp
 Quality coverage: 0.00x in Q20 bases; sum-of-contigs Quality
 coverage: 0.00x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 11 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 5636: contig of 5636 bp in length
 * 5637 5736: gap of 100 bp
 * 5737 17994: contig of 12258 bp in length
 * 17995 18094: gap of 100 bp
 * 18095 22433: contig of 4339 bp in length
 * 22434 22533: gap of 100 bp
 * 22534 50505: contig of 27972 bp in length
 * 50506 50605: gap of 100 bp
 * 50606 65269: contig of 14664 bp in length
 * 65270 65369: gap of 100 bp
 * 65370 67852: contig of 2483 bp in length
 * 67853 67952: gap of 100 bp
 * 67953 135901: contig of 67949 bp in length
 * 135902 136001: gap of 100 bp
 * 136002 147390: contig of 11389 bp in length
 * 147391 147490: gap of 100 bp
 * 147491 151011: contig of 3521 bp in length
 * 151012 151111: gap of 100 bp
 * 151112 163809: contig of 12698 bp in length
 * 163810 163909: gap of 100 bp
 * 163910 183911: contig of 20002 bp in length.

FEATURES

Source

1. 183911
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 /db_xref="taxon:9606"
 /chromosome="1"
 /clone="RP11-417D2"
 /clone.lib="RPC1-11.2"
 1. 5636
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 5737. 17994
 /note="assembly_fragment:00811.0"
 18095. 22433
 /note="assembly_fragment:01289.0"
 22534. 50505
 /note="assembly_fragment:01938.0"
 50606. 65269
 /note="assembly_fragment:03451.0"
 65370. 67852
 /note="assembly_fragment:03512.0"
 67953. 135901
 /note="assembly_fragment:03583.0"
 136002. 147390
 /note="assembly_fragment:03914.0"
 147491. 151011

misc_feature
 151112. 163809
 /note="assembly_fragment:06542.0"
 misc_feature
 163910. 183911
 /note="assembly_fragment:06790.0"
 BASE COUNT 51973 a 40172 c 39412 g 50869 t 1485 others
 ORIGIN

Query Match 16.5%; Score 138; DB 88; Length 183911;
 Best Local Similarity 100.0%; Pred. No. 8.2e-31;
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 - QY 582 caggacactctcgcagatcctctcttcttgcgtcgcgtcgcgttctctct 641
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 54421 CAGGACACTCTCGCAGATCACTCTCTTCTTCTGCGTGCCTGCTGCTCT 54480
 QY 642 tctcgtgttctctcctcgcgtcctctctctgtttaaaggcgagaaactcc 701
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 54481 TCTCTGTGTTCTCTCCACGCTCCGTTCTCTGTTCTTAAACGGGCAGAAACTCC 54540
 QY 702 tctatatattcaaacac 719
 ||||||||||||||||||||
 Db 54541 TGTATATATTCAACAAC 54558

RESULT 11

AC025220
 LOCUS AC025220 202773 bp DNA HTG 07-APR-2000
 DEFINITION Homo sapiens chromosome 1 clone RP11-281E22 map 1, WORKING DRAFT
 SEQUENCE, 35 unordered pieces.
 ACCESSION AC025220
 VERSION AC025220.2 GI:7523798
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 202773)
 Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 Unpublished
 2 (bases 1 to 202773)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
 Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
 Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,
 Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
 Collamore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
 Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
 Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
 Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
 Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
 Kleim,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J.,
 Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
 McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
 Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Menga,V., Morrow,J.,
 Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
 O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
 Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
 Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
 Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
 Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.
 Direct Submission

TITLE

JOURNAL
 Submitted (07-MAR-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Apr 7, 2000 this sequence version replaced gi:7188898.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

```

Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
-----
Project Information
Center project name: L8035
Center clone name: 281_E_22
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Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; Version: 9.60731
Consensus quality: 182912 bases at least Q40
Consensus quality: 192383 bases at least Q30
Consensus quality: 195712 bases at least Q20
Insert size: 217000; agarose-ftp
Quality coverage: 193373; sum-of-contigs
Quality coverage: 3.5 in Q20 bases; agarose-ftp
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 35 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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1 1182: contig of 1182 bp in length
1183 1282: gap of 100 bp
1283 2698: contig of 1416 bp in length
2699 2798: gap of 100 bp
2799 4194: contig of 1396 bp in length
4195 4294: gap of 100 bp
4295 5704: contig of 1410 bp in length
5705 5804: gap of 100 bp
5805 8389: contig of 2585 bp in length
8390 8489: gap of 100 bp
8490 10352: contig of 1863 bp in length
10353 10452: gap of 100 bp
10453 13024: contig of 2572 bp in length
13025 13124: gap of 100 bp
13125 15709: contig of 2385 bp in length
15710 15809: gap of 100 bp
15810 17470: contig of 1661 bp in length
17471 17570: gap of 100 bp
17571 20151: contig of 2581 bp in length
20152 20251: gap of 100 bp
20252 22870: contig of 2619 bp in length
22871 22970: gap of 100 bp
22971 25709: contig of 2739 bp in length
25710 25809: gap of 100 bp
25810 28338: contig of 2529 bp in length
28339 28438: gap of 100 bp
28439 32476: contig of 4038 bp in length
32477 32576: gap of 100 bp
32577 37518: contig of 4942 bp in length
37519 37618: gap of 100 bp
37619 41724: contig of 4106 bp in length
41725 41824: gap of 100 bp
41825 46408: contig of 4584 bp in length
46409 46508: gap of 100 bp
46509 51711: contig of 5203 bp in length
51712 51811: gap of 100 bp
51812 55860: contig of 5049 bp in length
55861 55960: gap of 100 bp
55961 62871: contig of 5911 bp in length
62872 62971: gap of 100 bp
62972 69111: contig of 6140 bp in length
69112 69211: gap of 100 bp
69212 75632: contig of 6421 bp in length
75633 75732: gap of 100 bp
75733 81565: contig of 5933 bp in length
81566 81665: gap of 100 bp
81666 88181: contig of 6516 bp in length

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/note="assembly_fragment"
81666..88181
/note="assembly_fragment"
88282..95593
/note="assembly_fragment"
95694..103809
/note="assembly_fragment"

Query Match
Best Local Similarity 16.1%; Score 134.8; DB 78; Length 202773;
Matches 139; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 445 ctggacaaactgtcttggatgaagtcgtgctgtgaaatggacgaagagagga 504
|||||
Db 44716 CTGCTAAGCTGTCTTGGATGGAAGCTGTGCTGTGTAATGGACGAGAGGGA 44775
|||||

QY 505 cgtggtctgtgacacatctccagctgacctctctccgggagacatctctgtgaccccgcc 564
|||||
Db 44776 CGTGGTCTGTGGACCATCTCCAGCCGACCTCTCTCGGGGAGCATCTCTGTGACCCGCC 44835
|||||

QY 565 taccctgcgagagaccagacact 590
|||||
Db 44836 TGCCCTGCGAGAGCCAGGTAAC 44861
|||||

RESULT 12
AC025225/c AC025225 162975 bp DNA HTG 07-JUL-2000
LOCUS Homo sapiens chromosome 1 clone RP11-12F19, WORKING DRAFT SEQUENCE,
DEFINITION 27 unordered pieces.
ACCESSION AC025225
VERSION AC025225.2 GI:7321916
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Waterston.R.H.
1 (bases 1 to 162975)
The sequence of Homo sapiens clone
Unpublished
JOURNAL
REFERENCE 2 (bases 1 to 162975)
AUTHORS Waterston.R.H.
TITLE Direct Submission
JOURNAL Submitted (07-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Mar 24, 2000 this sequence version replaced gi:7188903.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0012F19
----- Summary Statistics -----
Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 150748 bases at least Q40
Consensus quality: 15428 bases at least Q30
Consensus quality: 156305 bases at least Q20
Insert size: 166000; agarose-fp
Insert size: 160375; sum-of-contigs
Quality coverage: 3643.07 in Q20 bases; agarose-fp
Quality coverage: 3.83 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 27 contigs. The true order of the pieces
```

* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.

1
1217: contig of 1217 bp in length
1218 1317: gap of unknown length
1318 2463: contig of 1146 bp in length
2464 2564: gap of unknown length
2564 4498: contig of 1935 bp in length
4499 4599: gap of unknown length
4599 7094: contig of 2495 bp in length
7094 7194: gap of unknown length
7194 9954: contig of 2760 bp in length
9954 10054: gap of unknown length
10054 12618: contig of 2564 bp in length
12618 12718: gap of unknown length
12718 15058: contig of 2340 bp in length
15058 15158: gap of unknown length
15158 17781: contig of 2623 bp in length
17781 17881: gap of unknown length
17881 20007: contig of 2126 bp in length
20007 20107: gap of unknown length
20107 23039: contig of 2932 bp in length
23039 27294: gap of unknown length
27294 27394: contig of 4155 bp in length
27394 30128: gap of unknown length
30128 30228: contig of 2734 bp in length
30228 35378: gap of unknown length
35378 35478: contig of 5150 bp in length
35478 42408: gap of unknown length
42408 42509: contig of 6931 bp in length
42509 47863: gap of unknown length
47863 47963: contig of 5354 bp in length
47963 53784: gap of unknown length
53784 53884: contig of 5821 bp in length
53884 58405: gap of unknown length
58405 58505: contig of 4521 bp in length
58505 64501: gap of unknown length
64501 68823: contig of 5996 bp in length
68823 68923: gap of unknown length
68923 77163: contig of 4222 bp in length
77163 77264: gap of unknown length
77264 84281: contig of 8241 bp in length
84281 84380: gap of unknown length
84380 92444: contig of 7017 bp in length
92444 92544: gap of unknown length
92544 103799: contig of 8063 bp in length
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103800 103900: contig of 11256 bp in length
103900 116576: gap of unknown length
116576 129604: contig of 12676 bp in length
129604 129704: contig of 12928 bp in length
129704 143644: gap of unknown length
143644 143743: contig of 13940 bp in length
143743 162975: gap of unknown length
162975 19232: contig of 19232 bp in length.

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-12F19"
1..1217
/note="assembly_name:Contig10"
1318..2463
/note="assembly_name:Contig11"
2564..4498
/note="assembly_name:Contig12"
4599..7093
/note="assembly_name:Contig13"

misc_feature
1..1217
/note="assembly_name:Contig10"
1318..2463
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2564..4498
/note="assembly_name:Contig12"
4599..7093
/note="assembly_name:Contig13"

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misc_feature 7194..9953
/note="assembly_name:Contig14"
misc_feature 10054..12617
/note="assembly_name:Contig15"
misc_feature 12718..15057
/note="assembly_name:Contig16"
misc_feature 15158..17780
/note="assembly_name:Contig17"
misc_feature 17881..20006
/note="assembly_name:Contig18"
misc_feature 20107..23038
/note="assembly_name:Contig19"
misc_feature 23139..27293
/note="assembly_name:Contig20"
misc_feature 27394..30127
/note="assembly_name:Contig21"
clone_end:sp6
vector_side:left"
misc_feature 30228..35377
/note="assembly_name:Contig22"
misc_feature 35478..42408
/note="assembly_name:Contig23"
misc_feature 42509..47862
/note="assembly_name:Contig24"
misc_feature 47963..53783
/note="assembly_name:Contig25"
misc_feature 53884..58404
/note="assembly_name:Contig26"
misc_feature 58505..64500
/note="assembly_name:Contig27"
misc_feature 64601..68822
/note="assembly_name:Contig28"
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/note="assembly_name:Contig29"
misc_feature 77264..84280
/note="assembly_name:Contig30"
misc_feature 84381..92443
/note="assembly_name:Contig31"
misc_feature 92544..103799
/note="assembly_name:Contig32"
misc_feature 103900..116575
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misc_feature 116676..129603
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misc_feature 129704..143643
/note="assembly_name:Contig35"
misc_feature 143744..162975
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BASE COUNT 45139 a 35640 c 35357 g 44193 t 2646 others
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Best Local Similarity 92.0%; Pred. No. 2e-25;
Matches 127; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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|||||
Db 119307 CTTAAATTTTTTTTATGACATTTATGAGACCAGTCAAACTACTCAAGAGAGATGGC 119248
|||||

QY 761 tgtagctgccgattccagaagaagaagagagagatgtgaactgtgaatggaagtc 820
|||||
Db 119247 TGAGCTGCCGATTTTCAGAGAGAGAGAGAGAGAGATGTGAACCTGTAATGGAAGTCAA 119188
|||||

QY 821 taggctgttgggacttt 838
|||||
Db 119187 TAGGCTGTGGGACTTT 119170
|||||

RESULT 13
MMU02567
LOCUS MMU02567 12260 bp DNA ROD 30-MAR-1996
DEFINITION Mus musculus BALB/c T-cell antigen 4-1BB gene, complete cds.

```

```

ACCESSION U02567
VERSION U02567.1 GI:1117783
KEYWORDS mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (sites) Kwon,B.S., Kozak,C.A., Kim,K.K. and Pickard,R.T.
AUTHORS Genomic organization and chromosomal localization of the T-cell
TITLE antigen 4-1BB
JOURNAL J. Immunol. 152 (5), 2256-2262 (1994)
MEDLINE 94179805
REFERENCE 2 (bases 1 to 12260)
AUTHORS Kwon,B.S.
TITLE Direct Submission
JOURNAL Submitted (18-OCT-1993) Kwon B.S., Indiana University School of
Medicine, Microbiology and Immunology, 635 Barnhill Dr.,
Indianapolis, IN 46202, USA
COMMENT On Dec 14, 1995 this sequence version replaced gi:409177.
FEATURES
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location/Qualifiers
1..12260
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="P4-1BB"
/clone_lib="liver"
/germline
/sex="female"
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join(4934..5036,5933..6034,7502..7639,8225..8294,
9350..9404,9423..9495,10497..10628,11380..11477)
/codon_start=1
/product="T-cell antigen 4-1BB"
/protein_id="AAA93113.1"
/db_xref="GI:409178"
/translation="MGNNYVVVIVLLVGCCKVGVAVNSCDNCPETCRKYNVVC
KSGPPSTFSSIGGQPCNICRCVAGYFRFKFSSTHNAECIEGHCIGPQTRCE
KDCRPGQELFKQCKTCSLGTNDQNGTGVCRPTWNCSDGSRVLTGTFKDVVCGP
PVVSPSTTISVTPEGGPGHSLQVLTFLTALTSALLALIFITLLFSVLKWKRF
PHFKQPFKKTGAQEDACRCRCPQEEGGGGYEL"
BASE COUNT 3262 a 2773 c 2843 g 3382 t
ORIGIN

Query Match 8.6%; Score 72.2; DB 12; Length 12260;
Best Local Similarity 66.2%; Pred. No. 8.6e-11;
Matches 104; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 234 gcaggcagtgtaaagggtgttttcaggaccaggaaggagtggtctccaccagcaatgcag 293
|||||
Db 7487 GCTGGGCTTTGTAGGCTATTTTCAGGTTCAAGAAGTTTGTCTCTACCCACACGCG 7546
|||||

QY 294 agtgtagtcaactccagggtttcactgcctggggcaggatgcagatgtgtaacagg 353
|||||
Db 7547 AGTGAGTGCATTGAGGATTCATTGCTTGGGGCCACAGTCACCCAGATGTGAAAAGG 7606
|||||

QY 354 attgtaacaagggtcaagaactgacaaaaaggttg 390
|||||
Db 7607 ACTGCGCCCTGGCCAGGAGCTAACGAAGCAGGCTAG 7643
|||||

RESULT 14
I66494
LOCUS I66494 7218 bp DNA PAT 28-DEC-1997
DEFINITION Sequence 14 from patent US 5670367.
ACCESSION I66494
VERSION I66494.1 GI:2724471
KEYWORDS Unknown.
SOURCE Unclassified.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 7218)

```


GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 22, 2000, 03:39:41 : Search time 76.15 Seconds

(without alignments)
4134.016 Million cell updates/sec

Title: US-08-955-572-1

Perfect score: 838
Sequence: 1 aatcagcttgctagtatca.....aataggctgttggaacttt 838

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq.36:*

- 1: /cgn2_2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
- 2: /cgn2_2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
- 3: /cgn2_2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
- 4: /cgn2_2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
- 5: /cgn2_2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
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- 8: /cgn2_2/gcgdata/geneseq/geneseqn/NA1987.DAT:*
- 9: /cgn2_2/gcgdata/geneseq/geneseqn/NA1988.DAT:*
- 10: /cgn2_2/gcgdata/geneseq/geneseqn/NA1989.DAT:*
- 11: /cgn2_2/gcgdata/geneseq/geneseqn/NA1990.DAT:*
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- 21: /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	838	100.0	838	16	Q86126
2	836.4	99.8	838	17	T39546
3	836.4	99.8	1415	17	Q75424
4	836.4	99.8	1415	18	T91026
5	836.4	99.8	1439	20	Z09769
6	831.6	99.2	838	20	Z08961
7	828.4	98.9	1439	16	Q82086
8	608.8	72.6	946	18	T88969
9	608.8	72.6	946	20	X02162
10	339.2	40.5	2347	17	T39541
11	337.6	40.3	2350	16	O86127
12	337.6	40.3	2350	20	X80763

13	331.4	39.5	768	16	Q75428
14	331.4	39.5	768	18	T91027
15	36.4	4.3	2781	19	V62467
16	36.4	4.3	2853	20	X03846
17	35.8	4.3	3133	16	Q90652
18	34.8	4.2	1391	19	V41375
19	34.8	4.2	1391	19	V41369
20	34.8	4.2	3115	19	V41374
21	34.8	4.2	3115	19	V41368
22	34.8	4.2	3136	19	V41376
23	34.8	4.2	3136	19	V41370
24	34.8	4.2	3137	21	Z36257
25	34.8	4.2	3602	12	Q13849
26	34.2	4.1	10732	21	A10594
27	33.8	4.0	3816	20	Z32028
28	32	3.8	723	19	V19154
29	31.6	3.8	5059	20	X84332
30	31.6	3.8	15747	20	X13018
31	31.4	3.7	590	11	Q06353
32	31.4	3.7	2161	20	X03034
33	31.4	3.7	11901	20	X02998
34	31.2	3.7	2817	19	V57556
35	31.2	3.7	7156	19	V15586
36	31	3.7	2271	21	A37108
37	31	3.7	4067	15	Q63192
38	31	3.7	23503	19	V57926
39	31	3.7	237326	19	V57903
40	30.8	3.7	370	20	V87196
41	30.6	3.7	291	13	Q22192
42	30.6	3.7	291	13	Q32787
43	30.6	3.7	291	15	Q57810
44	30.6	3.7	291	19	V15526
45	30.6	3.7	847	20	Z33490

ALIGNMENTS

RESULT 1	
ID Q86126	standard; cDNA; 838 BP.
AC Q86126;	
DT 16-OCT-1995	(first entry)
XX	
DE H4-1BB receptor protein cDNA.	
DE	
XX	
KW H4-1BB; receptor protein; immunosuppressive; autoimmune disease;	
KW organ transplantation; cell membrane ligand; ss.	
OS Homo sapiens.	
XX	
FH Key	Location/Qualifiers
FT CDS	41..808
FT	/*tag= a
XX	
PN W09507984-A.	
XX	
PD 23-MAR-1995.	
XX	
PF 15-SEP-1994.	94MO-US10457.
XX	
PR 16-SEP-1993.	93US-0122796.
XX	
PA (INDV) UNIV INDIANA FOUND.	
XX	
PI Kwon BS.	
XX	
DR WPI: 1995-131352/17.	
DR P-PSDB: R70977.	
XX	
PT Novel cDNA encoding human receptor protein H4-1BB - useful to	

Murine 4-1BB polyp
Mouse 4-1BB recept
Human dendritic ce
Human tumour necro
Eph-related tyrosi
RANK partial polyp
RANK partial polyp
RANK partial polyp
RANK partial polyp
NF-kB receptor act
CDNA encoding a hu
A.niger pyruvate k
Gene encoding a su
Human MPTN relate
Truncated human 31
Stealth virus nucl
Enterococcus faeca
Exon 2 of ovine le
Human IL-1ra BAC c
Human IL-1ra BAC c
Rat Hrs-2 polypept
Lactobacillus bulg
Human PRO1604 (UNQ
Human adeno-associ
Hereditary haemoch
EST clone BN171.
Tetranucleotide re
Microsatellite rep
Repeat polymorphis
Polymorphic region
Human prostate can

PT produce the protein which is used to treat auto-immune disease
 PT and facilitate organ transplantation

XX Claim 2; Fig.2; 36pp; English.

CC Human peripheral blood lymphocyte-derived cDNA was amplified by PCR
 CC using probes based on the mouse receptor protein 4-1BB gene. The PCR
 CC product was used to screen a cDNA library of activated human T-cells.
 CC The isolated cDNA (Q86126), deposited as NRRL B21131, encoded the
 CC human homolog, H4-1BB (R70977), of 4-1BB.

XX Sequence 838 BP; 218 A; 191 C; 215 G; 214 T; 0 other;

Query Match 100.0%; Score 838; DB 16; Length 838;
 Best Local Similarity 100.0%; Pred. No. 2, 6e-262;
 Matches 838; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 aatcagcttctgtatcatcactgtgccaagattcatcatcgtggaacagctgtacaa 60
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Db 1 aatcagcttctgtatcatcactgtgccaagattcatcatcgtggaacagctgtacaa 60

QY 61 catagtagccactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 120
   |||||||
Db 61 catagtagccactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 120

QY 121 ttgtagtaactgcccagctgtgtacattctgtgataatacaggaatcagatttcagtc 180
   |||||||
Db 121 ttgtagtaactgcccagctgtgtacattctgtgataatacaggaatcagatttcagtc 180

QY 121 ttgtagtaactgcccagctgtgtacattctgtgataatacaggaatcagatttcagtc 180
   |||||||
Db 121 ttgtagtaactgcccagctgtgtacattctgtgataatacaggaatcagatttcagtc 180

QY 181 ctgtctcccaaatagttctccagcgagtgagcaaaagacctgtgacataatgacagca 240
   |||||||
Db 181 ctgtctcccaaatagttctccagcgagtgagcaaaagacctgtgacataatgacagca 240

QY 241 gtgtgaaagggttttccaggagcaaggagtggttcccccacacgaatgacagtgatga 300
   |||||||
Db 241 gtgtgaaagggttttccaggagcaaggagtggttcccccacacgaatgacagtgatga 300

QY 301 ctgacacccaggggttcaactgctcgtgagcgagatgacagatgctgtgacagagatga 360
   |||||||
Db 301 ctgacacccaggggttcaactgctcgtgagcgagatgacagatgctgtgacagagatga 360

QY 301 ctgacacccaggggttcaactgctcgtgagcgagatgacagatgctgtgacagagatga 360
   |||||||
Db 301 ctgacacccaggggttcaactgctcgtgagcgagatgacagatgctgtgacagagatga 360

QY 361 acaaggtcacaagaactgacaaaagaagtgtaagaactgtgtgtgtgtgtgtgtgtgt 420
   |||||||
Db 361 acaaggtcacaagaactgacaaaagaagtgtaagaactgtgtgtgtgtgtgtgtgtgt 420

QY 421 tcaagaacgttgacatcgtgtgacaccttgacaaactgttcttggatggaagctgtgtct 480
   |||||||
Db 421 tcaagaacgttgacatcgtgtgacaccttgacaaactgttcttggatggaagctgtgtct 480

QY 481 tgtgaatgaggaaggaaggaaggaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 540
   |||||||
Db 481 tgtgaatgaggaaggaaggaaggaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 540

QY 541 gggagacatcctgtgtgaccccgctgcccctgcgagagagccaggaacatctccgcagat 600
   |||||||
Db 541 gggagacatcctgtgtgaccccgctgcccctgcgagagagccaggaacatctccgcagat 600

QY 601 catctctctcttctgtgacgtgacgtgacgtgtgtgtgtgtgtgtgtgtgtgtgtgt 660
   |||||||
Db 601 catctctctcttctgtgacgtgacgtgacgtgtgtgtgtgtgtgtgtgtgtgtgtgt 660

QY 661 gctccgttctctgtgtttaaagcgaggaagaagaactcctgtatataatcaaacacc 720
   |||||||
Db 661 gctccgttctctgtgtttaaagcgaggaagaagaactcctgtatataatcaaacacc 720

QY 721 attatagaaccagtaacaaactcaagaaggaagatggtgtgtgtgtgtgtgtgtgt 780
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Db 721 attatagaaccagtaacaaactcaagaaggaagatggtgtgtgtgtgtgtgtgtgt 780

QY 781 agagaagaaggaaggaatgtgaactgtgaatgaatgaatgaatgaatgaatgaatgaat 838
   |||||||
Db 781 agagaagaaggaaggaatgtgaactgtgaatgaatgaatgaatgaatgaatgaatgaat 838

```

RESULT 2

T39546 standard; cDNA to mRNA; 838 BP.

T39546;

12-DEC-1996 (first entry)

Human receptor H4-1BB cDNA.

Receptor 4-1BB; H4-1BB; monoclonal antibody; T-lymphocyte; T-cell;

immunostimulant; cancer; autoimmune disease; graft rejection;

therapy; ss.

Homo sapiens.

Key Location/Qualifiers

CDS 41..808

mat_peptide 41..805

W09629348-A1.

26-SEP-1996.

22-MAR-1996; 96WO-US03965.

23-MAR-1995; 95US-0409851.

(INDV) UNIV INDIANA FOUND.

Kang C, Kwon BS;

WPI; 1996-443138/44.

P-PSDB; W04174.

Monoclonal antibody specific for human receptor protein 4-1BB - used

to enhance proliferation and activation of T-cells for treatment of

cancer and to inhibit specific ligand binding for treating

auto-immune diseases

Disclosure; Page 36-37; 48pp; English.

A cDNA clone (T39546) codes for novel human receptor protein

H4-1BB (W04174), a protein that has the potential to function as

an accessory signaling molecule during T-cell activation and

proliferation. The cDNA clone was isolated from a lambda gt11

cDNA library of activated human T lymphocytes by screening with a

PCR product obd. by amplification of lymphocyte cDNA using

primers (see also T39542-45) based on the murine 4-1BB cDNA

(T39541). It can be used to produce recombinant H4-1BB useful

for isolating H4-1BB ligands, for stimulating proliferation of

B-cells expressing H4-1BB ligands, for blocking H4-1BB ligand

binding and for raising anti-H4-1BB monoclonal antibody.

Sequence 838 BP; 218 A; 192 C; 214 G; 214 T; 0 other;

Query Match 99.8%; Score 836.4; DB 17; Length 838;
 Best Local Similarity 99.9%; Pred. No. 8, 8e-262;
 Matches 837; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 aatcagcttctgtatcatcactgtgccaagattcatcatcgtggaacagctgtacaa 60
   |||||||
Db 1 aatcagcttctgtatcatcactgtgccaagattcatcatcgtggaacagctgtacaa 60

QY 61 catagtagccactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 120
   |||||||
Db 61 catagtagccactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 120

```

```
QY 121 ttgtaagtaactgccagctgtacattctgtgataataacagaagatctgcagctcc 180
    |||
Db 121 ttgtagtaactgcccagctgtgtacattctgtgataataacagaagatctgcagctcc 180
QY 181 ctgtccctccaaatagttctccagcgaggtgagcaaaagacctgtgacatgcaagca 240
    |||
Db 181 ctgtccctccaaatagttctccagcgaggtgagcaaaagacctgtgacatgcaagca 240
QY 241 gtttaaaagtgtttccagagccagaagagtggttccctccacagcaatgcagaagtga 300
    |||
Db 241 gtttaaaagtgtttccagagccagaagagtggttccctccacagcaatgcagaagtga 300
QY 301 ctgcacccacagaggtttcaacgacctgggggagagatgtagatgtgtaaaagatttaa 360
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Db 301 ctgcacccacagaggtttcaacgacctgggggagagatgtagatgtgtaaaagatttaa 360
QY 361 acaaggctcaagaactgacaaanaaaaggtgtgaaagactgtgtcttggagcatgtaacga 420
    |||
Db 361 acaaggctcaagaactgacaaanaaaaggtgtgaaagactgtgtcttggagcatgtaacga 420
QY 421 tcagaaacgttgcatctgttcgacccctggacaacactgttcttgatggaagtctgtgct 480
    |||
Db 421 tcagaaacgttgcatctgttcgacccctggacaacactgttcttgatggaagtctgtgct 480
QY 481 tgtgaatggagcagaagagagagagctgtgtctgtggaccatctccagctcctctcc 540
    |||
Db 481 tgtgaatggagcagaagagagagagctgtgtctgtggaccatctccagctcctctcc 540
QY 541 gggagcatctctgtgaccccgctgccccttgagagagacagagacactctccagat 600
    |||
Db 541 gggagcatctctgtgaccccgctgccccttgagagagacagagacactctccagat 600
QY 601 catctcctctctctgtcgctgcagctgcagctgcgtgctctctcctgcttctctccac 660
    |||
Db 601 catctcctctctctgtcgctgcagctgcagctgcgtgctctctcctgcttctctccac 660
QY 661 gctcccttctctgtgtttaaaggcgagaaagaaactcctgtatatataataaacacc 720
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Db 661 gctcccttctctgtgtttaaaggcgagaaagaaactcctgtatatataataaacacc 720
QY 721 attatagagaccagtaacaaactactcaagagagagatgctgtgtagctgcgattccaga 780
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Db 721 attatagagaccagtaacaaactactcaagagagagatgctgtgtagctgcgattccaga 780
QY 781 agaagaagaagagagatgtagactgtgaaatggaagtaacaaatagagctgtgtggaactt 838
    |||
Db 781 agaagaagaagagagatgtagactgtgaaatggaagtaacaaatagagctgtgtggaactt 838

RESULT 3
ID Q75424 standard; cDNA to mRNA; 1415 BP.
XX
AC Q75424;
XX
DT 08-AUG-1995 (first entry)
XX
DE Human 4-1BB polypeptide coding sequence.
XX
KW T-cell; lymphocyte; activation; tissue culture; clone; cell lines;
KM proliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 120..887
FT /tag= a
FT /product= 4-1BB polypeptide.
FT sig_peptide 120..188
FT /tag= b
FT mat_peptide 189..884
FT /tag= c
XX
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PN W09426290-A.
XX
PD 24-NOV-1994.
XX
PF 06-MAY-1994; 94MO-US05036.
XX
PR 07-MAY-1993; 93US-0060843.
XX
PA (IMMUNEX CORP.
PI Alderson MR, Goodwin RG, Smith CA;
XX
XX WPI: 1995-022265/03.
DR P-PSDB; R64197.
XX
PT Cytokine, 4-1BB ligand (4-1BB-L) - binds to cell surface receptor
PS Claim 29; Page 46-47; 65pp; English.
XX
XX The 4-1BB polypeptide (receptor) and the 4-1BB-L (cytokine, see
CC Q75423) are useful in a pharmaceutical composition for stimulating
CC the immune system. The 4-1BB and 4-1BB-L polypeptides are also useful
CC for exploring mechanisms of T-cell activation, as they are expressed
CC on T lymphocytes. 4-1BB-L can be used as a tissue culture reagent for
CC in vitro cultivation of primary T-cells during the derivation of
CC clonal T-cell lines. It may also be used to stimulate proliferation
XX of activated T-cells, used in therapeutic procedures.
XX
SQ Sequence 1415 BP; 385 A; 332 C; 333 G; 365 T; 0 other;
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Query Match 99.8%; Score 836.4; DB 16; Length 1415;
Best Local Similarity 99.9%; Pred. No. 1.2e-261;
Matches 837; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 aatgaagtttgctgtatataactgtgcccagatttcataatgggaaacagctgttaaa 60
    |||
Db 80 aatgaagtttgctgtatataactgtgcccagatttcataatgggaaacagctgttaaa 139
QY 61 catagtggccactgtgtgtgtgtcctcaactttgagagagacaagatattgcagagatcc 120
    |||
Db 140 catagtggccactgtgtgtgtgtcctcaactttgagagagacaagatattgcagagatcc 199
QY 121 ttgtagtaactgcccagctgtgtacattctgtgataataacagaagatctgcagctcc 180
    |||
Db 200 ttgtagtaactgcccagctgtgtacattctgtgataataacagaagatctgcagctcc 259
QY 181 ctgtcctccaaatagttctccagcgaggtgagcaaaagacctgtgacatgcaagca 240
    |||
Db 260 ctgtcctccaaatagttctccagcgaggtgagcaaaagacctgtgacatgcaagca 319
QY 241 gttgaaagggtgtttccagagcagaagagtggttccctccacagcaatgtagagtgga 300
    |||
Db 320 gttgaaagggtgtttccagagcagaagagtggttccctccacagcaatgtagagtgga 379
QY 301 ctgcacccacagaggtttcaactgacctgggggagagatgtagactgtgttggagcatgtaacga 360
    |||
Db 380 ctgcacccacagaggtttcaactgacctgggggagagatgtagactgtgttggagcatgtaacga 439
QY 361 acaaggctcaagaactgacaaanaaaaggtgtgaaagactgtgtcttggagcatgtaacga 420
    |||
Db 440 acaaggctcaagaactgacaaanaaaaggtgtgaaagactgtgtcttggagcatgtaacga 499
QY 421 tcagaaacgttgcatctgttcgacccctggacaacactgttcttgatggaagtctgtgct 480
    |||
Db 500 tcagaaacgttgcatctgttcgacccctggacaacactgttcttgatggaagtctgtgct 559
QY 481 tgtgaatggagcagaagagagagagctgtgtctgtggaccatctccagctcctctcc 540
    |||
Db 560 tgtgaatggagcagaagagagagagctgtgtctgtggaccatctccagctcctctcc 619
QY 541 gggagcatctctgtgaccccgctgccccttgagagagacagagacactctccagat 600
```

```

|||||
Db 620 ggagcaccctctgtgaccccgccgcccgcgagagaccagacacctccgcagat 679
QY 601 catcctctctctctgtgcgtgacgtgactgctgtctctccgcgtctctctaac 660
Db 680 catcctctctctctgtgcgtgacgtgactgctgtctctccgcgtctctctaac 739
QY 661 gtcctgtctctctgtgttaaacgggagagaagaactcctgtatataatcaaac 720
Db 740 gtcctgtctctctgtgttaaacgggagagaagaactcctgtatataatcaaac 799
QY 721 attatgagaccagtaacaaactactcaagagagaatgctgtagctgcgattccaga 780
Db 800 attatgagaccagtaacaaactactcaagagagaatgctgtagctgcgattccaga 859
QY 781 agaaagaagaagatgtgactgtgaactggaatcaatagggctgttgagactt 838
Db 860 agaaagaagaagatgtgactgtgaactggaatcaatagggctgttgagactt 917

RESULT 4
T91026
ID T91026 standard; cDNA to mRNA, 1415 BP.
XX
AC T91026;
XX
DT 25-FEB-1998 (first entry)
XX
DE Human 4-1BB receptor cDNA clone hu4-1BB.
XX
KW 4-1BB ligand; 4-1BB-L; receptor; human; cytokine; T lymphocyte;
KW T cell; proliferation; immunostimulant; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 120..887
FT FT /*tag= a
FT sig_peptide 120..188
FT FT /*tag= b
FT mat_peptide 189..884
FT FT /*tag= c
XX
XX US5674704-A.
XX
XX PD 07-OCT-1997.
XX
XX PF 07-MAY-1993; 93US-0060843.
XX
XX PR 06-MAY-1994; 94US-0236918.
XX PR 07-MAY-1993; 93US-0060843.
XX
XX PA (IMMV ) IMMUNEX CORP.
XX
XX PI Alderson MR, Goodwin RG, Smith CA;
XX
XX DR WPI: 1997-502333/46.
XX DR P-PSDB; W26658.
XX
XX PT DNA encoding 4-1BB ligand polypeptide(s) - useful for stimulating
XX PT T-cell proliferation in vitro, and as research tools
XX
XX PS Example 2; Column 43-46; 32pp: English.
XX
XX This cDNA clone encodes human 4-1BB (see W26658), a member of the
XX tumour necrosis factor receptor superfamily that is expressed on
XX cells that include, but are not limited to, stimulated human
XX peripheral blood lymphocytes. The clone was isolated from a cDNA
XX library prepared from human peripheral blood T-lymphocytes that
XX had been activated with phytohemagglutinin and phorbol myristate
XX acetate. A fragment of murine 4-1BB DNA (see T91027) was used
XX as probe. A novel claimed cytokine, designated 4-1BB ligand
XX (4-1BB-L) has been identified, cloned and sequenced (see W26657)

```

CC that binds to 4-1BB. 4-1BB-L, especially its soluble extracellular
 CC domain, can be used to stimulate T-cell proliferation in vitro, as
 CC a research tool and as an affinity ligand for purifying 4-1BB.
 XX
 SQ Sequence 1415 BP; 385 A; 332 C; 333 G; 365 T; 0 other;

Query Match 99.8%; Score 836.4; DB 18; Length 1415;
 Best Local Similarity 99.9%; Pred. NO. 1.2e-261;
 Matches 837; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 aatcagcttctgtatcatcaactctgtgcagattcatcatatggaagaagctgttaaca 60
Db 80 aatcagcttctgtatcatcaactctgtgcagattcatcatatggaagaagctgttaaca 139
QY 61 catatagaccactcgtgtgtctgtcctcaactttagagggagaataatcatcagaatcc 120
Db 140 catatagaccactcgtgtgtctgtcctcaactttagagggagaataatcatcagaatcc 199
QY 121 ttgtatgactgcccagctgtgtacattctgtatataatacagaagaatcagatttcagttcc 180
Db 200 ttgtatgactgcccagctgtgtacattctgtatataatacagaagaatcagatttcagttcc 259
QY 181 ctgtccctccaaatagttctcctcagcgcaggtgagacaagaagacctgtgacatatgcagga 240
Db 260 ctgtccctccaaatagttctcctcagcgcaggtgagacaagaagacctgtgacatatgcagga 319
QY 241 ggttaagtggttttcagagaccaggaagagtgcttcctccaccagaatgcagatgtga 300
Db 320 ggttaagtggttttcagagaccaggaagagtgcttcctccaccagaatgcagatgtga 379
QY 301 ctgcactcagaaggttccactgctcgtgggcaagatgcagacatgtgtgaacagatgtga 360
Db 380 ctgcactcagaaggttccactgctcgtgggcaagatgcagacatgtgtgaacagatgtga 439
QY 361 acaaggtcaagaactcgcacaaanaaagtgtaagaactgtgtcttggagacatttaaca 420
Db 440 acaaggtcaagaactcgcacaaanaaagtgtaagaactgtgtcttggagacatttaaca 499
QY 421 tcaagaagctgcatctgtgcacccctgcgaacaacgttcttggatggaatcctgtgtc 480
Db 500 tcaagaagctgcatctgtgcacccctgcgaacaacgttcttggatggaatcctgtgtc 559
QY 481 tctgaatggagaaaggagagagacgtgtgtgtgacatccagctgacactctctcc 540
Db 560 tctgaatggagaaaggagagagacgtgtgtgtgacatccagctgacactctctcc 619
QY 541 ggagacatcctctgtgaccccgctgcctcgcagagagacaggaacactccgcagat 600
Db 620 ggagacatcctctgtgaccccgctgcctcgcagagagacaggaacactccgcagat 679
QY 601 catcctctctctctgtgcgtgacgtgactgctgtctctccgcgtctctctaac 660
Db 680 catcctctctctctgtgcgtgacgtgactgctgtctctccgcgtctctctaac 739
QY 661 gtcctgtctctctgtgttaaacgggagagaagaactcctgtatataatcaaac 720
Db 740 gtcctgtctctctgtgttaaacgggagagaagaactcctgtatataatcaaac 799
QY 721 attatgagaccagtaacaaactactcaagagagaatgctgtagctgcgattccaga 780
Db 800 attatgagaccagtaacaaactactcaagagagaatgctgtagctgcgattccaga 859
QY 781 agaaagaagaagatgtgactgtgaactggaatcaatagggctgttgagactt 838
Db 860 agaaagaagaagatgtgactgtgaactggaatcaatagggctgttgagactt 917

RESULT 5
209769
ID Z09769 standard; cDNA; 1439 BP.
XX
AC Z09769;

```

XX 18-NOV-1999 (first entry)
XX
DE Human CD137 cDNA.
XX
KW CD137; monocyte growth factor; proliferation; peripheral monocyte;
KW treatment; disease; antitumor; antibacterial; antiviral; antifungal;
KW immunostimulatory; non-specific immune response; phagocytosis;
KW intracellular destruction; microorganism; immune complex; antibody;
KW cytotoxicity; tumor cell; macrophage; hematopoietic system; leucopenia;
KW chemotherapy; radiation; therapy; wound healing disorder; tumor; fungal;
KW bacterial; viral infection; immunosuppressant; gene therapy; human; ds.
XX
OS Homo sapiens.
FH
FT Key Location/Qualifiers
FT CDS 140..907.
FT /tag="a
FT /product="CD137"
XX
XX WO944629-A2.
XX
XX 10-SEP-1999.
XX
XX 05-MAR-1999; 99MO-EP01440.
XX
XX 05-MAR-1998; 98EP-0103859.
XX
XX (MERC) MERCKLE GMBH.
XX
XX Schwarz H, Langstein J;
XX WPI: 1999-550983/46.
XX P-PSDB: Y33214.
XX
XX Use of monocyte growth factor CD137 for stimulating proliferation of
XX peripheral monocytes, particularly for treating immune deficiency, e.g.
XX following cancer therapy -
XX
XX Disclosure: Flg 1A; 57pp; German.
XX
XX This invention describes a novel use of the human monocyte growth factor
XX CD137, or its functional analogs, for (i) stimulating proliferation of
XX peripheral monocytes; and (ii) treating diseases that are associated with
XX disorders of a cellular system that includes monocytes (and/or their
XX derived cells, precursor or progenitors) or where the origin and/or
XX progression is treatable by stimulating proliferation of such cells. The
XX products of the invention have antitumor, antibacterial, antiviral,
XX antifungal and immunostimulatory activity. Stimulating proliferation of
XX monocytes promotes the non-specific immune response, i.e. It increases
XX phagocytosis and intracellular destruction of microorganisms. Immune
XX complexes and damaged cells, and improves antibody (in)dependent
XX cytotoxicity to tumor cells. CD137 is used, in vivo or ex vivo, to treat
XX diseases associated with a defective immune response where caused by
XX inadequate numbers of active monocytes/macrophages, especially damage to
XX the hematopoietic system (leucopenia) caused by chemotherapy or radiation
XX therapy; disorders of wound healing (e.g. in dialysis or diabetic
XX patients, or those with chronic venous insufficiency); tumors; bacterial,
XX fungal or viral infections; (non-)congenital or (non-)inherited diseases
XX or injury to the immune system; injury induced by treatment with
XX immunosuppressants (e.g. patients with chronic arthritis or autoimmune
XX disease, or transplant patients). Nucleic acid encoding (I) can be used
XX similarly, in gene therapy procedures. Proliferation of peripheral
XX monocytes is achieved independently of hematopoietic stem cells. This
XX sequence encodes the human CD137 protein described in the method of
XX the invention.
XX
XX Sequence 1439 BP: 394 A: 340 C: 341 G: 364 T: 0 other:

Query Match 99.8%; Score 836.4; DB 20; Length 1439;
Best Local Similarity 99.9%; Pred. No. 1.2e-261;
Matches 837; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 aatcagcttctgctagatcatacctctgtccagatttcatactggaagaacgctgttaca 60
DB 100 aatcagcttctgctagatcatacctctgtccagatttcatactggaagaacgctgttaca 159
QY 61 catagtagccactctgttctgttcccaacttggaggaacaagatcatctgacagatcc 120
DB 160 catagtagccactctgttctgttcccaacttggaggaacaagatcatctgacagatcc 219
QY 121 ttgtaatactgcccgctgttaccatctctgtataataaagaatcagaattgtgcattcc 180
DB 220 ttgtaatactgcccgctgttaccatctctgtataataaagaatcagaattgtgcattcc 279
QY 181 ctgtccccaatagatttctccagcgagtggaacaagaacctgtgacatagtcaagca 240
DB 280 ctgtccccaatagatttctccagcgagtggaacaagaacctgtgacatagtcaagca 339
QY 241 gtgtaaagggtttttagagacaggaagagtgcttctccacgaatgcaagagtgtga 300
DB 340 gtgtaaagggtttttagagacaggaagagtgcttctccacgaatgcaagagtgtga 399
QY 301 ctgcactccaagggttccactgtccctggggcaagatgcaagatgtgtgacaagatgttaa 360
DB 400 ctgcactccaagggttccactgtccctggggcaagatgcaagatgtgtgacaagatgttaa 459
QY 361 acaaggccaagaacttgacaacaaaagggtgtaaagaactgtgtcttggacatttaagca 420
DB 460 acaaggccaagaacttgacaacaaaagggtgtaaagaactgtgtcttggacatttaagca 519
QY 421 tcagaagaactgtgcatctgttcgaacctggacaacactgttcttggatggaaagtctgtct 480
DB 520 tcagaagaactgtgcatctgttcgaacctggacaacactgttcttggatggaaagtctgtct 579
QY 481 tgtgaatggagcaagaagagagacgtgtgtctgttgacacatcccaagctgactctcc 540
DB 580 tgtgaatggagcaagaagagagacgtgtgtctgttgacacatcccaagctgactctcc 639
QY 541 gggagacatctctgtgaccccgctgcctctggagagagccagacatctccgagat 600
DB 640 gggagacatctctgtgaccccgctgcctctggagagagccagacatctccgagat 699
QY 601 catctctcttcttctgtgcgtgacgtgcagctggtgtcttctctctctctccac 660
DB 700 catctctcttcttctgtgcgtgacgtgcagctggtgtcttctctctctctccac 759
QY 661 gctcgttctctctgttgaacggggcagaagaacactccttatatatccaacaacc 720
DB 760 gctcgttctctctgttgaacggggcagaagaacactccttatatatccaacaacc 819
QY 721 attatgagaccagtaacaaactactcaagaagagaatggtctgtagctccgattccaga 780
DB 820 attatgagaccagtaacaaactactcaagaagagaatggtctgtagctccgattccaga 879
QY 781 aagaagaagaagagatgtgactgtgaatggaatgaatgaggtgttggaactt 838
DB 880 aagaagaagaagagatgtgactgtgaatggaatgaatgaggtgttggaactt 937
RESULT 6
ID 208961 standard; cDNA: 838 BP.
XX 208961;
XX
XX 13-OCT-1999 (first entry)
XX
XX Human receptor protein 4-1BB cDNA.
XX
XX Human receptor protein 4-1BB; H4-1BB; T cell activation; proliferation;
XX mouse 4-1BB cDNA; monoclonal antibody; immune response;
XX organ transplantation; autoimmune disease; diabetes; cancerous tumour;
XX rheumatoid arthritis; lupus; nerve growth factor receptor; ds.

[illegible]

Dd		361	acaagctcaagaactgcacaaaaaaagggttctaagaactggttgctttgggacatttaacga	420
Qy		421	tcaagaagaatggcatctcgtcgacccttgacaacaactgtcttccttgatbtgaagtctgtgc	480
Dd		421	tcaagaagaatggcatctcgtcgacccttgacaacaactgtcttccttgatbtgaagtctgtgc	480
Qy		481	tgtgaatggagcagaagagagagagcgttgtctctgtgacacatccacgtcacctctccc	540
Dd		481	tgtgaatggagcagaagagagagagcgttgtctctgtgacacatccacgtcacctctccc	540
Qy		541	gggaacatccctctctgacccccctgccccctgcagagagccaggaacctctccagat	600
Dd		541	gggaacatccctctctgacccccctgccccctgcagagagccaggaacctctccagat	600
Qy		601	cattccctctctctctgagccctgcagatgcgtctgctctctccctctgctctctccac	660
Dd		601	cattccctctctctctgagccctgcagatgcgtctgctctctccctctgctctctccac	660
Qy		661	gtccgcttctctctgtgtttaacgggggcagaagaanaacctctgtatatataatcaaacac	720
Dd		661	gtccgcttctctctgtgtgtttaacgggggcagaagaanaacctctgtatatataatcaaacac	720
Qy		721	atttatgagaccagtacacaactactccaagaggaagatgctgttagctgtccgatcttcaga	780
Dd		721	atttatgagaccagtacacaactactccaagaggaagatgctgttagctgtccgatcttcaga	780
Qy		781	agaagaagaagagagatgtgactgtgaatgaatgaatcataatgaagctgtgtggaactt	838
Dd		781	agaagaagaagagagatgtgactgtgaatgaatgaatcataatgaagctgtgtggaactt	838
RESULT 7				
ID	O92086		O92086 standard; DNA; 1439 BP.	
XX	AC	O92086;		
DT	21-JAN-1996	(first entry)		
DE		Human receptor induced by lymphocyte activation (ILA) DNA.		
KM	IL4; receptor inducible by lymphocyte activation; disease diagnosis;			
KW	antInflammatory; ss.			
OS	Homo sapiens.			
FH	Key	Location/Qualifiers		
FT	CDS	140..904		
FT		/*tag= a		
PN	CA2108401-A.			
PD	28-MAR-1995.			
PF	14-OCT-1993;	93CA-2108401.		
PR	27-SEP-1993;	93US-0127693.		
PA	(REGC) UNIV CALIFORNIA.			
PI	Lotz M, Schwarz H;			
DR	WPI; 1995-194420/26.			
DR	P-PsDB; R74087.			
PT	New receptor inducible by lymphocyte activation - used to develop			
PS	prods. for the diagnosis and treatment of inflammatory host defence			
CC	pathology.			
CS	Claim 52; Page 61; 91pp; English.			
CC	This DNA may be expressed recombinantly for the production of IL4.			
CC	The cDNA was isolated from a library constructed from activated			

CC human T-lymphocyte leukemia virus type-1 transformed human T-
 CC lymphocytes.
 XX
 SQ Sequence 1439 BP; 393 A; 336 C; 346 G; 364 T; 0 other;

Query Match 98.9%; Score 828.4; DB 16; Length 1439;
 Best Local Similarity 99.3%; Pred. No. 4.8e-259;
 Matches 832; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 aatcagcttgtagatatacctgtgcagattcatcatatggaacagctgttaca 60
 |||||||
 DB 100 aatcagcttgtagatatacctgtgcagattcatcatatggaacagctgttaca 159
 QY 61 catagtagcactctgtctgtctcctaactttgagagacaagatcatcagaatcc 120
 |||||||
 DB 160 catagtagcactctgtctgtctcctaactttgagagacaagatcatcagaatcc 219
 QY 121 ttgttagtaactgccagcgtgatactctgtataataacaggaatcagatttgacgcc 180
 |||||||
 DB 220 ttgttagtaactgccagcgtgatactctgtataataacaggaatcagatttgacgcc 279
 QY 181 ctgtctcccaatagttcttcacagcaggtgacacaagagacctgtgacatatgcagaca 240
 |||||||
 DB 280 ctgtctcccaatagttcttcacagcaggtgacacaagagacctgtgacatatgcagaca 339
 QY 241 gtgtaaagggttttcaaggacagaagagtgcttctccacacagcaatgcagatgtga 300
 |||||||
 DB 340 gtgtaaagggttttcaaggacagaagagtgcttctccacacagcaatgcagatgtga 399
 QY 301 ctgcacatccagaggttctacatgctggggcagatgacagatgtgtgaacagatgttaa 360
 |||||||
 DB 400 ctgcacatccagaggttctacatgctggggcagatgacagatgtgtgaacagatgttaa 459
 QY 400 ctgcacatccagaggttctacatgctggggcagatgacagatgtgtgaacagatgttaa 459
 |||||||
 DB 361 acaaggtcacaagactgcacaaaaaaggtgttaagacgttgccttggagacatttaaga 420
 |||||||
 DB 460 acaaggtcacaagactgcacaaaaaaggtgttaagacgttgccttggagacatttaaga 519
 QY 421 tcaagaacgttgcatctgtgcacccctgcacaaactgttcttggatgtaaaatctgtgtc 480
 |||||||
 DB 520 tcaagaacgttgcatctgtgcacccctgcacaaactgttcttggatgtaaaatctgtgtc 579
 QY 481 ttgtgaatggagaggaaggaagagtgctgtgacacatccagctgcactctcc 540
 |||||||
 DB 580 ttgtgaatggagaggaaggaagagtgctgtgacacatccagctgcactctcc 639
 QY 541 gggaacatcctctgtgaccccgctgccttcgagagagcagagacactcccgagat 600
 |||||||
 DB 640 gggaacatcctctgtgaccccgctgccttcgagagagcagagacactcccgagat 699
 QY 601 catctcctcttcttctgcgtgcagctgcagctgtgtccttctcctgcac 660
 |||||||
 DB 700 catctcctcttcttctgcgtgcagctgcagctgtgtccttctcctgcac 759
 QY 661 gctcgttcttctgtgttaaacgggacagaagaacactcgtatataatcaaacacc 720
 |||||||
 DB 760 gctcgttcttctgtgttaaacgggacagaagaacactcgtatataatcaaacacc 819
 QY 721 attatgacacagatcacaaactcacaaagagaatggctgtagctgcagatttcaga 780
 |||||||
 DB 820 attatgacacagatcacaaactcacaaagagaatggctgtagctgcagatttcaga 879
 QY 781 aagaagaagaagagatgtgaactgtgaatggaagtcataatgaggtcgttggacttt 838
 |||||||
 DB 880 aagaagaagaagagatgtgaactgtgaatggaagtcataatgaggtcgttggacttt 937

RESURF 8
 ID T88969 standard; DNA; 946 BP.
 XX
 AC T88969;
 XX

DT 01-APR-1998 (first entry)
 XX
 DE DNA encoding a human h4-1BSV receptor.
 XX
 XX h4-1BSV receptor; 4-1BB receptor splicing variant; endotoxic shock;
 KW tumour necrosis factor; TNF ligand; T-cell activation; inflammation;
 KW tumour prevention; viral infection; autoimmune disease;
 KW cellular proliferation; ss.
 XX
 OS Homo sapiens.
 OS
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 124..783
 FT /tag= a
 FT sig_peptide 124..177
 FT /tag= b
 FT /note= "putative"
 FT mat_peptide 178..780
 FT /tag= c
 XX
 PN WO9733898-A1.
 XX
 PD 18-SEP-1997.
 XX
 XX
 PF 15-MAR-1996; 96WO-US03587.
 XX
 PR 15-MAR-1996; 96WO-US03587.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Gentz RL, Ni J, Yu G;
 XX
 XX WPI; 1997-470806/43.
 DR P-PSDB; W31759.
 XX
 PT Human 4-1BB receptor splicing variant and related DNA - used to
 PT develop products for treating e.g. tumours, viral infection,
 PT endotoxick shock, autoimmune disease or bone resorption.
 PS
 PS
 CC Claim 8; Fig 1; 73pp; English.
 CC
 CC The present sequence encodes a novel human h4-1BSV receptor. This is a
 CC human 4-1BB receptor splicing variant. The 4-1BB ligand is a member of
 CC the tumour necrosis factor (TNF) family of ligands. It is induced by
 CC T-cell activation. The h4-1BSV receptor nucleic acid and protein can be
 CC used for diagnosis and therapy. In particular, agonists of h4-1BSV
 CC receptor can be used to treat and/or prevent tumours, restenosis,
 CC cytotoxicity, bacterial and viral infection, deleterious effects of
 CC ionising radiation, autoimmune disease, AIDS and graft-host rejection,
 CC to regulate immune responses, wound healing and cellular proliferation.
 CC Antagonists can be used to treat and/or prevent endotoxick shock,
 CC inflammation, cerebral malaria, activation of the HIV virus, graft
 CC rejection, bone resorption and cachexia.
 CC
 CC
 SQ Sequence 946 BP; 257 A; 218 C; 230 G; 241 T; 0 other;

Query Match 72.6%; Score 608.8; DB 18; Length 946;
 Best Local Similarity 86.9%; Pred. No. 9.1e-188;
 Matches 728; Conservative 0; Mismatches 2; Indels 100; Gaps 1;

QY 1 aatcagcttgtagatatacctgtgcagattcatcatatggaacagctgttaca 60
 |||||||
 DB 84 aatcagcttgtagatatacctgtgcagattcatcatatggaacagctgttaca 143
 QY 61 catagtagcactctgtctgtctcctaactttgagagacaagatcatcagaatcc 120
 |||||||
 DB 144 catagtagcactctgtctgtctcctaactttgagagacaagatcatcagaatcc 203
 QY 121 ttgttagtaactgccagcgtgatactctgtgataataacaggaatcagatttgacgcc 180
 |||||||
 DB 204 ttgttagtaactgccagcgtgatactctgtgataataacaggaatcagatttgacgcc 222

```
QY 181 ctgtccccaatagtttctccagcgaggtgacaagaacctgtacatatcgagca 240
Db 223 -----
QY 241 gtgtaaagtgatttcaggaccaggaaagagtggtctccccaacgacatgcagagtga 300
Db 223 -----gggttttcaggaccaggaaagagtggtctccccaacgacatgcagagtga 275
QY 301 ctgacaccagggttctactgctctggggcagagatgcagacatgtgtgaacagagttaa 360
Db 276 ctgacaccagggttctactgctctggggcagagatgcagacatgtgtgaacagagttaa 335
QY 361 acaaggtcaagaactgcacaaaagaagtttgaagaactgtgtgtgttggaattaa 420
Db 336 acaaggtcaagaactgcacaaaagaagtttgaagaactgtgtgtgttggaattaa 395
QY 421 tcgaaaacgtgcatctgtgcaccccttgacaactgtttcttgatgtgaagtgtgct 480
Db 396 tcgaaaacgtgcatctgtgcaccccttgacaactgtttcttgatgtgaagtgtgct 455
QY 481 tgtgaatggagacgaaggagagagcgtgtctgtgagaccatctcagctgacctctcc 540
Db 456 tgtgaatggagacgaaggagagagcgtgtctgtgagaccatctcagctgacctctcc 515
QY 541 gggagcatcctctgtgaccccgctgcacctgcagagagcaggaacatctccgagat 600
Db 516 gggagcatcctctgtgaccccgctgcacctgcagagagcaggaacatctccgagat 575
QY 601 catctcctctcttcttgctgcgtgacgtgcagctgtgtctctctgctgttctctccac 660
Db 576 catctcctctcttcttgctgcgtgacgtgcagctgtgtctctctgctgttctctccac 635
QY 661 gctcgttctctgtgtttaaaccgggcaagaagaacatctcgtatataatcaacaacc 720
Db 636 gctcgttctctgtgtttaaaccgggcaagaagaacatctcgtatataatcaacaacc 695
QY 721 attatgagaccagtaacaactactcaagaagagatgtgtgtagctgtgcgattccaga 780
Db 696 attatgagaccagtaacaactactcaagaagagatgtgtgtagctgtgcgattccaga 755
QY 781 agaaagaagaagagatgtgtaactgtgaatggaatgaatgaaggctgtgttgacctt 838
Db 756 agaaagaagaagagatgtgtaactgtgaatggaatgaatgaaggctgtgttgacctt 813

RESULT 9
X02162
ID X02162 standard; DNA; 946 BP.
XX
AC X02162;
XX
DT 23-APR-1999 (first entry)
XX
DE Human h4-1BBSV receptor DNA.
XX
KW h4-1BBSV receptor; human; splice variant; antagonist; treatment;
KW disease prevention; endotoxic shock; inflammation; cerebral malaria;
KW HIV virus activation; graft rejection; bone resorption; cachexia;
KW gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key 124..783 Location/Qualifiers
FT CDS 124..783
FT /tag= a
FT /product= "h4-1BBSV"
FT sig_peptide 124..177
FT /tag= b
FT mat_peptide 178..780
FT /tag= c
XX
PN US5874240-A.
XX
```

```
PD 23-FEB-1999.
XX
PF 13-MAR-1997; 9705-0816605.
XX
PR 15-MAR-1996; 96US-0013474.
PR 13-MAR-1997; 97US-0816605.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI DILLON PJ, Gentz R, Ni J, Yu G;
DR WPI: 1999-179974/15.
DR P-PSDB; W92523.
XX
PT New nucleic acid encoding human 4-1BB receptor splicing variant -
PT useful in treating h4-1BBSV mediated disease states such as
PT endotoxic shock, inflammation, graft rejection and inactivation of
PT HIV
XX
PS Claim 11; Fig 1A-B; 28pp; English.
XX
CC This sequence encodes a novel human h4-1BBSV receptor protein which is
CC used in a method for making a human 4-1BB receptor splice variant which
CC acts as an antagonist. The antagonist polypeptides may be used to
CC treat/prevent disease states mediated by h4-1BBSV receptors such as
CC endotoxic shock, inflammation, cerebral malaria, activation of the HIV
CC virus, graft rejection, bone resorption and cachexia. The h4-1BBSV
CC coding sequences are useful in gene therapy.
XX
SQ Sequence 946 BP; 257 A; 218 C; 230 G; 241 T; 0 other:

Query Match 72.6%; Score 608.8; DB 20; Length 946;
Best Local Similarity 86.9%; Pred. No. 9.1e-188;
Matches 728; Conservative 0; Mismatches 2; Indels 108; Gaps 1;

QY 1 aatcagcttgctgatacatcctgtgcagatltcaatcattgaggaacagctgttaca 60
Db 84 aatcagcttgctgatacatcctgtgcagatltcaatcattgaggaacagctgttaca 143
QY 61 catgtgagccactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 120
Db 144 catgtgagccactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 203
QY 121 ttgtagtactgcccagctgtgtacatctcgtgtgataatacaggaatcagatttcag 180
Db 204 ttgtagtactgcccagctgtgtacatctcgtgtgataatacaggaatcagatttcag 222
QY 181 ctgtccccaatagtttctccagcgaggtgacaagaacctgtgacatatcgagca 240
Db 223 -----
QY 241 gtgtaaagtgatttcaggaccaggaaagagtggtctccccaacgacatgcagagtga 300
Db 223 -----gggttttcaggaccaggaaagagtggtctccccaacgacatgcagagtga 275
QY 301 ctgacaccagggttctactgctctggggcagagatgcagacatgtgtgaacagagttaa 360
Db 276 ctgacaccagggttctactgctctggggcagagatgcagacatgtgtgaacagagttaa 335
QY 361 acaaggtcaagaactgcacaaaagaagtttgaagaactgtgtgtgttggaattaa 420
Db 336 acaaggtcaagaactgcacaaaagaagtttgaagaactgtgtgtgttggaattaa 395
QY 421 tcgaaaacgtgcatctgtgcaccccttgacaactgtttcttgatgtgaagtgtgct 480
Db 396 tcgaaaacgtgcatctgtgcaccccttgacaactgtttcttgatgtgaagtgtgct 455
QY 481 tgtgaatggagacgaaggagagagcgtgtctgtgagaccatctcagctgacctctcc 540
Db 456 tgtgaatggagacgaaggagagagcgtgtctgtgagaccatctcagctgacctctcc 515
QY 541 gggagcatcctctgtgaccccgctgcacctgcagagagcaggaacatctccgagat 600
```



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DE 4-1BB receptor protein cDNA.
XX
KM 4-1BB; receptor protein; immunosuppressive; autoimmune disease;
KM organ transplantation; cell membrane ligand; ss.
XX
OS Mus sp.
XX
XX Key Location/Qualifiers
FH CDS 146..916
FT sig_peptide 146..214
FT mat_peptide 215..913
FT /*tag= c
FT /*product= 4-1BB receptor protein
FT misc_difference 1253..1255
FT /*tag= d
FT /*note= "bases n at positions 1253-1255 are not
FT polyA_signal 1303..1308 identified in the specification"
FT /*tag= e
XX
XX WO9507984-A.
XX
XX PD 23-MAR-1995.
XX
XX PF 15-SEP-1994; 94WO-US10457.
XX
XX PR 16-SEP-1993; 93US-0122796.
XX
XX (INDV ) UNIV INDIANA FOUND.
XX
XX PA
XX PI
XX P1
XX Kwon BS;
XX
XX DR WPI: 1995-131352/17.
XX DR P-PSDB; R70978.
XX
XX DR
XX PT Novel cDNA encoding human receptor protein H4-1BB - useful to
XX PT produce the protein which is used to treat auto-immune disease
XX PT and facilitate organ transplantation
XX
XX PS Disclosure; Fig.1; 36pp; English.
XX
XX CC PCR primers based on the mouse receptor protein 4-1BB gene, given in
XX CC O86127, were used to probe a cDNA library of activated human T-cells
XX CC to isolate the homologous human gene, H4-1BB (O86126).
XX
XX SO Sequence 2350 BP; 590 A; 559 C; 591 G; 607 T; 3 other:

Query Match 40.3%; Score 337.6; DB 16; Length 2350;
Best Local Similarity 67.7%; Pred. No. 2.2e-99;
Matches 536; Conservative 0; Mismatches 244; Indels 12; Gaps 4;

```

```

OY 314 ttccatcgtcgtgggacagatgcatgtgtgaaacagatgtgtaaacaggtcaagaa 373
DB 416 ttccatcgtcgtgggacacagatgtcaaccagatgtgtaaaagatcagagcctggcagag 475
OY 374 ctgacaaaaaaggtgtgtaaaagatgtgtctgttgagacatttaacgatacagaacg---t 430
DB 476 ctacgaagcagaggtgtgcaaaacctgtagcttgggaacatttaacgatacagaacgtaact 535
OY 431 ggcacgtgtgacccctggaacacacgtctcttggatggaaagtcgtgtctgtgtaatgg 490
DB 536 ggggtctgtgcacccctggaacacacgtctcttgaacggaaggtgtgtgttaagaacggg 595
OY 491 acgaaggaagagcagtgctgtgtggaacatccagacgtcactctcccggaagcacc 550
DB 556 accaaggaaggaagcagtggtgtgtggaacccctgtgtgtgagcttctcccaag---tacc 652
OY 551 tctgtgaaccccgctgcacctgagagagacagacacactccgacagatcatctccttc 610
DB 653 accattctgtgactccagaggaaggaaggaaggaaggaaggaaggaaggaaggaaggaag 712
OY 611 ttctgtgctgacgtgacgtgtgtgtcttctccgtgttcttcttaagctccgttc 670
DB 713 ttcctggcgtgacatcg---gcttgcgtgcgtgcctgcatcttcatctctcgttgc 769
OY 671 tctgtgttaaacgggacgaagaagaactcctgtatataatcaaacacacattatgaga 730
DB 770 tctgtgctcaaatgtgatacgaagaataatccccacatatcaagaacacatttaagaag 829
OY 731 ccagtaacaactactcaagaagaagatgtgtgtagctgcggaattccagaagaagaaga 790
DB 830 accactggagcagcctcaagaagaagatgtgtgtagctgcggaattccagaagaagaaga 889
OY 791 ggaagatgtgaa 802
DB 890 ggaagagaagga 901

RESULT 12
X90763
ID X90763 standard; cDNA; 2350 BP.
XX
XX AC X90763;
XX
XX DT 13-OCT-1999 (first entry)
XX
XX DE Mouse receptor protein 4-1BB cDNA.
XX
XX KW Mouse receptor protein 4-1BB cDNA; 4-1BB receptor protein;
KW H4-1BB protein; human 4-1BB protein; T cell activation; proliferation;
KW immune response; autoimmune disease; organ transplantation;
KW cancerous tumour; ss.
XX
XX OS Mus musculus.
XX
XX FH Key Location/Qualifiers
XX FT CDS 146..916
XX FT /*tag= a
XX FT /*product= "Mouse 4-1BB receptor protein"
XX
XX WO9936093-A1.
XX
XX PD 22-JUL-1999.
XX
XX PF 14-JAN-1999; 99WO-US00823.
XX
XX PR 14-JAN-1998; 98US-0007097.
XX
XX PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.
XX PA (KWON/) KWON B S.
XX
XX PI Kwon BS;
XX

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DR WPI: 1999-444325/37.
DR P-PSDB: Y28687.

PT Using human receptor protein 4-1BB ligands to, e.g. treat Diabetes
PT Mellitus, Rheumatoid Arthritis and Systemic Lupus Erythematosus
XX
XX
PS Disclosure; Page 74-75; 86pp; English.

CC The present sequence encodes mouse 4-1BB receptor protein. This protein
CC has 65% homology with human receptor protein 4-1BB. Probes derived from
CC mouse 4-1BB cDNA are used to isolate cDNA of H4-1BB. The H4-1BB protein,
CC its ligands, and various monoclonal antibodies have therapeutic uses.
CC They may be used to enhance or suppress T cell activation and
CC proliferation; for activation or inhibition of immune response; to block
CC H4-1BB ligand binding; treating cancerous tumours and autoimmune
CC diseases; and during organ transplantation.

XX
SQ Sequence 2350 BP; 590 A; 562 C; 589 G; 606 T; 3 other;

Query Match 40.3%; Score 337.6; DB 20; Length 2350;
Best Local Similarity 67.7%; Pred. No. 2.2e-99;
Matches 536; Conservative 0; Mismatches 244; Indels 12; Gaps 4;

QY 14 agatataactctgccaagattcatcatggaagaagcgtgtacacatagtagccact 73
DB 119 aggtccctgtgcatgacattccgcattggaacaacacgttacaacgtagtgcatt 178
QY 74 ctgtctgtgtccctcaactttagagagacacatcatctgagatcccttgaactgc 133
DB 179 gtgtctgtctagtagtggtctgtgagaaggtgagcgctgagacactcctgtgaactgc 238
QY 134 ccagctggtatcattctgtgataataacagaatcagatttgcagtcctctccaat 193
DB 239 cagctctgtactcttctgcagaataatc--aatccagctgcagaagctgcctcccaagt 295
QY 194 agttctccagcgacgtgtagcaagaagcctgtgacatacagcgacgagcttaaggtgt 253
DB 296 accttcccgacataagtgagacacgacgaactgtacaacatccgcagagtgtagcaggtat 355
QY 254 ttcaagacaggaagagtgcttctccacacgaatgcagatgtgactcactccaggg 313
DB 356 ttcaagttcaagaagatttgctctctaccacaacgcgagtgtagtgatctgaagga 415
QY 314 ttcaactgcttgaggagacagatgtgtgaacagagattgtataacaaagttcaagaa 373
DB 416 ttcaattgtcttgaggacacagtgaccagatgtgaagaagacgcagcgtgctgcagga 475
QY 374 ctgaacaaaaaagtgtagaagactgttgccttgggaacatttaacgatacgaagc--t 430
DB 476 ctacaagagcaggtgtgcaaaacctgtgacttgggaacatttaacgacgaacgctact 535
QY 431 ggcattctgacccctgggaacaaactgttcttggatggaagactgtgcttgaatggg 490
DB 536 gggctctgtgcacctgggaacaaactgtctcttagacggaaggtctgtgtctaaagccgg 595
QY 491 acgaagaagagagagctgtgtctgtgacacatctcagcttcaactctctccggagacatcc 550
DB 596 accaagagagagagagctgtgtgtgtgagacccctgtgtgtgactctccacag--tacc 652
QY 551 tctgtgaacccgcctgcacctgcagagagacggaacactctccgagatcatctcctc 610
DB 653 accatttctgtgactccagagagagacggaagggacactcttgcagcttcaacttg 712
QY 611 ttctctgagctgagcgtgacatgctgtctctcctgtgtcttccccaacgcctgtt 670
DB 713 ttctctgagctgacatgc--gttctgtctgtgtgacctgtcttcttcaatctccctt 769
QY 671 tctgtgttaaacggtgagcaagaacatccctgtatataattcaacaacacattatgaga 730
DB 770 tctgtgtcaaatgtagtcaagaaaatccccaacataattcaagcaacatttaagaag 829
QY 731 ccagttacaacactcaagaagagagatggtctgtgactgcccgaattccagaagaagaag 790

DB 830 accactggagcagctcaagaagagagatgctgtgactgcccgaatgccacaggaagaagaa 889
QY 791 ggaagatgtgaa 802
DB 890 ggaagagagagga 901

RESULT 13

ID Q75428 standard; cDNA to mRNA; 768 BP.

AC Q75428;

DT 08-AUG-1995 (first entry)

DE Murine 4-1BB polypeptide coding sequence.

KW T-cell; lymphocyte; activation; tissue culture; clone; cell lines;

KW proliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine; ss.

OS Mus musculus.

FN Key Location/Qualifiers

FT CDS 1..768

FT sig_peptide 1..69

FT mat_peptide 70..768

PN WO9426290-A.

PD 24-NOV-1994.

PF 06-MAY-1994; 94MO-US05036.

PR 07-MAY-1993; 93US-0060843.

PA (IMMUNEX) IMMUNEX CORP.

PI Alderson MR, Goodwin RG, Smith CA;

DR WPI: 1995-022265/03.

DR P-PSDB: R64199.

PT Cytokine, 4-1BB ligand (4-1BB-L) - binds to cell surface receptor

PT 4-1BB to transduce signal

PS Example 1; Page 43-44; 65pp; English.

XX The 4-1BB polypeptide (receptor) and the 4-1BB-L (cytokine, see

CC Q75428) are useful in a pharmaceutical composition for stimulating

CC the immune system. The 4-1BB and 4-1BB-L polypeptides are also useful

CC for exploring mechanisms of T-cell activation, as they are expressed

CC on T lymphocytes. 4-1BB-L can be used as a tissue culture reagent for

CC in vitro cultivation of primary T-cells during the derivation of

CC clonal T-cell lines. It may also be used to stimulate proliferation

CC of activated T-cells, used in therapeutic procedures.

XX
SQ Sequence 768 BP; 188 A; 186 C; 217 G; 177 T; 0 other;

Query Match 39.5%; Score 331.4; DB 16; Length 768;
Best Local Similarity 68.2%; Pred. No. 1.2e-97;
Matches 522; Conservative 0; Mismatches 231; Indels 12; Gaps 4;

QY 41 atgggaacacgctgttacaacatagtagcactctgtgtgctgtcctcaacttgagagg 100
DB 1 atgggaacacacgtttacaacagtggtgtgtcattgtgtctgtctagtggtggtgagag 60
QY 101 acaagatcatgtcagagctctttagtaactgtccacagctgtgtatctctgtgataaac 160

QY 638 ctctctcgtgtcttctcctcagctccggttctctgttgaacgggagagaaga 697
 || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 592 ctgttgccctgattcattcattcctctctgtctgtctcaatgataagaaaaa 651
 QY 698 ctctgtatatatcaacaacacattatgagaccaggtacaactactcaagaagaat 757
 || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 652 ttcccccaatttcaagcaacatttaagaagacgtgagcctcaagaagaagat 711
 QY 758 ggcgtgagcgcgatttccagagaagaagaagaagtgtgaa 802
 | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 712 gctgtgagcgtgctgattccacagagaagaagaagaagaaga 756
 RESULT 15
 V62467
 ID V62467 standard; cDNA; 2781 BP.
 AC V62467;
 XX
 DT 21-JAN-1999 (first entry)
 DE Human dendritic cell receptor protein encoding cDNA.
 XX
 KM Receptor protein; ligand: therapeutic agent; breast cancer; AIDS;
 KM prostate cancer; ovarian cancer; follicular lymphoma; p53 mutation;
 KM brain tumour; bladder carcinoma; cervical cancer; intestinal cancer;
 KM lung cancer; gastric cancer; herpesvirus; adenovirus; poxvirus; human;
 KM H. pylori infection; varicella-zoster virus; human papillomavirus;
 KM staphylococcal; influenza virus; systemic mycosis; bacterial pneumonia;
 KM bacterial peritonitis; viral encephalitis; diabetes mellitus; sepsis;
 KM adult respiratory distress syndrome; leukaemia; malignant melanoma;
 KM multiple myeloma; non-Hodgkin lymphoma; peptic ulcer; septic shock;
 KM tuberculosis; immunological disease; dermatitis; allergic rhinitis;
 KM pollen allergy; inflammation; arthritis; hepatitis; autoimmune disease;
 KM rheumatoid arthritis; disseminated lupus erythematosus; bronchial asthma;
 KM Sjogren's disease; glomerulonephritis; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT sig_peptide 19..105
 FT /tag= a
 FT 19..1869
 FT CDS
 FT /tag= b
 FT /product= "receptor protein"
 FT 106..648
 FT /tag= c
 FT /note= "sequence coding for a partial soluble peptide"
 FT mat_peptide 106..1866
 FT /tag= d
 XX
 XX
 PN BP873998-A2.
 XX
 XX 28-OCT-1998.
 XX
 PF 24-APR-1998; 98BP-0303190.
 XX
 XX 17-SEP-1997; 97JP-0251867.
 PR 25-APR-1997; 97JP-0109798.
 XX
 XX (TAKE) TAKEDA CHEM IND LTD.
 PA
 PI Horiguchi T, Nishi K, Shintani A;
 XX
 DR WPI: 1998-544608/47.
 DR P-PSDB; W79233.
 XX
 PT New dendritic cell receptor belonging to TNF receptor family - used
 PT to treat e.g. cancer, AIDS, bacterial and viral infections,
 PT insulin-dependent diabetes mellitus, peptic ulcer, sepsis, septic
 PT shock and allergic immunological disorders
 XX

PS Disclosure: Fig 1; 65pp; English.

XX This represents the nucleotide sequence of a receptor protein derived
 CC from a human dendritic cell. The receptor protein or its fragment or
 CC salt can be used to determine a ligand to it, and for screening a
 CC compound which alters binding properties between it and a ligand. The
 CC compound is used for therapeutic purposes. The therapeutic agents are
 CC used to treat cancer (breast cancer, prostate cancer, ovarian cancer,
 CC follicular lymphoma, cancer accompanied by p53 mutation, brain tumour,
 CC bladder carcinoma, cancer of uterine cervix, cancer of large intestine
 CC (carcinoma of colon and rectum), non-small and small cell lung cancer
 CC and gastric cancer). AIDS, infections (e.g. herpesvirus, adenovirus,
 CC poxvirus, H. pylori, varicella-zoster virus, human papillomavirus,
 CC active, staphylococcal and influenza virus infections and severe systemic
 CC mycosis), acute bacterial peritonitis, acute viral encephalitis, adult
 CC respiratory distress syndrome, bacterial pneumonia, chronic lymphocytic
 CC leukaemia, chronic myelogenous leukaemia, insulin-dependent diabetes
 CC mellitus (type 1), malignant melanoma, multiple myeloma, non-Hodgkin
 CC lymphoma, peptic ulcer, sepsis, septic shock, tuberculosis, allergic
 CC immunological diseases (e.g. atopic dermatitis, contact dermatitis,
 CC allergic rhinitis and pollen allergy), inflammation (e.g. arthritis and
 CC hepatitis), autoimmune diseases (e.g. rheumatoid arthritis, disseminated
 CC lupus erythematosus and Sjogren's disease), glomerulonephritis and
 CC bronchial asthma.
 CC
 SQ Sequence 2781 BP; 585 A; 811 C; 778 G; 607 T; 0 other.

Query Match

4.3%; Score 36.4; DB 19; Length 2781;

Best Local Similarity 61.7%; Pred. No. 0.2; Matches 58; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 431 ggcattctgcaccctgacacaaactgtcttctgagagaagctgtgtgaaatgg 490
 || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 517 gacaaatgcagaccctgacacaaactgtcttctgagagaagctgtgtgaaatgg 576
 QY 491 acgaagagagagagcgtgtgtctgtgacacatc 524
 || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 577 acagagaatcgcattgtgtgtgagctctctc 610

Search completed: November 22, 2000, 05:34:24
 Job time: 6883 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 22, 2000, 00:49:40 ; Search time 61.81 Seconds
(Without alignments)
2050.483 Million cell updates/sec

Title: US-08-955-572-1

Sequence: 1 aatcagcttgcctagatca.....aataggcttggtgactt 838

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 262060 seqs, 75620727 residues

Total number of hits satisfying chosen parameters: 524120

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.NA:*
1: /cgn2_6/prodata/2/lna/5A_COMB.seq:*
2: /cgn2_6/prodata/2/lna/5B_COMB.seq:*
3: /cgn2_6/prodata/2/lna/5C_COMB.seq:*
4: /cgn2_6/prodata/2/lna/5D_COMB.seq:*
5: /cgn2_6/prodata/2/lna/5E_COMB.seq:*
6: /cgn2_6/prodata/2/lna/PCrns_COMB.seq:*
7: /cgn2_6/prodata/2/lna/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	838	100.0	838	6	PCT-US94-10457-1
2	838	100.0	838	6	PCT-US96-03965-7
3	836.4	99.8	1415	1	US-08-236-918A-7
4	608.8	72.6	946	3	US-08-816-605-1
5	339.2	40.5	2347	6	PCT-US96-03965-1
6	331.4	39.5	768	1	US-08-236-918A-5
7	45.6	5.4	7218	1	US-08-232-463-14
8	42.2	5.0	7218	1	US-08-232-463-14
9	35.8	4.3	1333	1	US-08-162-809-1
10	34.8	4.2	1391	5	US-08-996-139-3
11	34.8	4.2	3115	5	US-08-996-139-5
12	34.8	4.2	3136	5	US-08-996-139-5
13	32	3.8	723	5	US-08-911-423-5
14	31.4	3.7	152331	5	US-09-128-155-16
15	31.4	3.7	176373	5	US-09-128-155-17
16	31	3.7	4060	1	US-08-308-949A-1
17	31	3.7	246240	3	US-08-724-394A-20
18	31	3.7	246240	3	US-08-724-394A-21
19	31	3.7	246240	3	US-08-724-394A-22
20	30.6	3.7	291	1	US-07-922-723A-7
21	30.6	3.7	291	1	US-07-922-723A-7
22	30.6	3.7	291	1	US-08-074-275-7
23	30.6	3.7	291	2	US-08-480-366-7
24	30.4	3.6	12127	5	US-07-952-277A-7
25	30.4	3.6	12127	5	US-08-444-644-32
26	30	3.6	30	4	US-08-859-998-420

27	29.6	3.5	6256	3	US-08-475-891A-1	Sequence 1, Appl1
28	29.6	3.5	6256	4	US-08-567-375-1	Sequence 1, Appl1
29	29.6	3.5	6256	4	US-08-587-680A-1	Sequence 1, Appl1
30	29.4	3.5	3918	5	US-08-836-329-1	Sequence 1, Appl1
31	29.2	3.5	363	4	US-08-966-316-8	Sequence 8, Appl1
32	29	3.5	1558	2	US-08-487-823B-1	Sequence 1, Appl1
33	29	3.5	1558	4	US-08-997-040-1	Sequence 1, Appl1
34	29	3.5	1558	4	US-09-203-237-1	Sequence 1, Appl1
35	29	3.5	1564	5	US-08-948-997-1	Sequence 1, Appl1
36	28.8	3.4	2652	3	US-08-766-738-2	Sequence 1, Appl1
37	28.8	3.4	2652	3	US-08-366-547-1	Sequence 1, Appl1
38	28.6	3.4	519	4	US-08-249-189-4	Sequence 4, Appl1
39	28.6	3.4	519	4	US-08-484-624A-4	Sequence 4, Appl1
40	28.6	3.4	519	4	US-08-477-733B-4	Sequence 4, Appl1
41	28.6	3.4	519	5	US-09-088-913A-4	Sequence 4, Appl1
42	28.6	3.4	1318	2	US-08-419-009-27	Sequence 27, Appl1
43	28.6	3.4	1358	2	US-08-419-009-29	Sequence 29, Appl1
44	28.6	3.4	1436	2	US-08-419-009-28	Sequence 28, Appl1
45	28.6	3.4	1435	2	US-08-419-009-26	Sequence 26, Appl1

ALIGNMENTS

RESULT 1
PCT-US94-10457-1
; Sequence 1, Application PC/TUS9410457
; GENERAL INFORMATION:
; APPLICANT: Byong Se Kwon
; TITLE OF INVENTION: New Human Receptor and Related Products
; NUMBER OF INVENTION: and Methods
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Barnard & Brown
; STREET: 306 E. State St., Suite 220
; CITY: Ithaca
; STATE: New York
; COUNTRY: United States
; ZIP: 14850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; OPERATING SYSTEM: IBM AT Compatible
; SOFTWARE: Special Obasic program
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10457
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/012,269
; FILING DATE: 2/1/93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/922,996
; FILING DATE: 7/30/92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/267,577
; FILING DATE: 11/7/88
; ATTORNEY/AGENT INFORMATION:
; NAME: Michaels, Christopher A.
; REGISTRATION NUMBER: 34,350
; REFERENCE/DOCKET NUMBER: kmh41dbb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 607-273-1711
; TELEFAX: 607-273-2609
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 838
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEICAL: NO

ANTI-SENSE: NO
FRAGMENT TYPE: n/a
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
INDIVIDUAL ISOLATE: H4-1BB #1
DEVELOPMENTAL STAGE: Differentiated T-cell
HAPLOTYPE:
TISSUE TYPE: Lymphocytes
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY: cDNA library
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: H4-1BB
LOCATION:
IDENTIFICATION METHOD: Similarity to mouse 4-1BB and other
IDENTIFICATION METHOD: members of NCFR superfamily
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: Kwon, B.S., and Weissman, S.M.
TITLE: cDNA sequences of two inducible T-cell genes
JOURNAL: Proc. Natl. Acad. Sci. USA
VOLUME: 86
ISSUE:
PAGES: 1963-1967
RELEVANT RESIDUES IN SEQ ID NO: all
PCT-US94-10457-1

Query Match 100.0%; Score 838; DB 6; Length 838;
Best Local Similarity 100.0%; Pred. No. 9.7e-251;
Matches 838; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aatgaagcttctgtagtatacctgctgacagattctatcgtgaaacagctgttaca 60
DB 1 aatgaagcttctgtagtatacctgctgacagattctatcgtgaaacagctgttaca 60
QY 61 catagtagccactctgtctgctcctcaactttgagaggaacaagatctgcaagatcc 120
DB 61 catagtagccactctgtctgctcctcaactttgagaggaacaagatctgcaagatcc 120
QY 121 ttgtagtaactgcccagctggtacattctgtgataataacaggaatcagatttcagtc 180
DB 121 ttgtagtaactgcccagctggtacattctgtgataataacaggaatcagatttcagtc 180
QY 181 ctgtccctcccaatagtttctccagcgagtgagacaagaagaccgtgtgacatgtgagca 240
DB 181 ctgtccctcccaatagtttctccagcgagtgagacaagaagaccgtgtgacatgtgagca 240
QY 241 gtgtaaaggttcttccagagcagaagagtggttcccccacacagcaatgcaagtgatga 300
DB 241 gtgtaaaggttcttccagagcagaagagtggttcccccacacagcaatgcaagtgatga 300
QY 301 ctgactcagaaggttctcactgctgagggcagatgacagcatgtgtgacagagattgtaa 360
DB 301 ctgactcagaaggttctcactgctgagggcagatgacagcatgtgtgacagagattgtaa 360
QY 361 acaaggtcaagaactgacaaaaaaggtgttaagagctgtgtcttggagacatttaaga 420
DB 361 acaaggtcaagaactgacaaaaaaggtgttaagagctgtgtcttggagacatttaaga 420
QY 421 tcagaaagctgtgcatctctgacccctgagcaaaactgttcttggatggaagagctgtgct 480
DB 421 tcagaaagctgtgcatctctgacccctgagcaaaactgttcttggatggaagagctgtgct 480
QY 481 tgtgaatggagcagaagagagagcgtgtgtgtgacacatctccagctgacctctctcc 540

DB 481 tctgaatggagcagaagagagagcgtgtgtgtgacacatctccagctgacctctctcc 540
QY 541 ggaagcattctctgtgaccccgccctgctgagagagcagaagcagactctccagat 600
DB 541 ggaagcattctctgtgaccccgccctgctgagagagcagaagcagactctccagat 600
QY 601 catctcctcttctctgtgctgacgtcagctgctgtctctctcgtcttctctcag 660
DB 601 catctcctcttctctgtgctgacgtcagctgctgtctctctcgtcttctctcag 660
QY 661 gctccgttctctgtgtgttaaacgggcaagaagaactcctgtatataatcaaacac 720
DB 661 gctccgttctctgtgtgttaaacgggcaagaagaactcctgtatataatcaaacac 720
QY 721 attatgagaccagfacacactcaagagagagatgctgtagctccgattccaga 780
DB 721 attatgagaccagfacacactcaagagagagatgctgtagctccgattccaga 780
QY 781 agaagaagaagagagatgtgaactgtgaatgtgaagtcataagagctgtgagactt 838
DB 781 agaagaagaagagagatgtgaactgtgaatgtgaagtcataagagctgtgagactt 838

RESULT 2
PCT-US96-03965-7
Sequence 7, Application PC/TUS9603965
GENERAL INFORMATION:
APPLICANT: Kwon, Byoung Se
TITLE OF INVENTION: Monoclonal antibody against human
TITLE OF INVENTION: receptor 4-1BB
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Barnard, Brown & Michaels
STREET: 306 East State Street, Suite 220
CITY: Ithaca
STATE: NY
COUNTRY: USA
ZIP: 14850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03965
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,796
FILING DATE: 16-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012,269
FILING DATE: 01-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/922,996
FILING DATE: 30-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/267,577
FILING DATE: 07-NOV-1988
ATTORNEY/AGENT INFORMATION:
NAME: Michaels, Christopher A
REGISTRATION NUMBER: 34,390
TELECOMMUNICATION INFORMATION:
TELEPHONE: 607-273-1711
TELEFAX: 607-273-2609
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 838 base pairs
TYPE: nucleic acid
STRANDEDNESS: double


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?       TOPOLOGY: linear
?       MOLECULE TYPE: cDNA to mRNA
?       HYPOTHETICAL: NO
?       ANTI-SENSE: NO
?       ORIGINAL SOURCE:
?       ORGANISM: Homo sapiens
?       INDIVIDUAL ISOLATE: H4-1BB #1
?       DEVELOPMENTAL STAGE: Differentiated T-cell
?       CELL TYPE: Lymphocyte
?       FEATURE:
?       NAME/KEY: CDS
?       LOCATION: 41..805
?       OTHER INFORMATION: /codon_start= 41
?       OTHER INFORMATION: /product= "H4-1BB"
?       OTHER INFORMATION: /number= 1
?       FEATURE:
?       NAME/KEY: mat_peptide
?       LOCATION: 41..802
?       OTHER INFORMATION: /codon_start= 41
?       OTHER INFORMATION: /product= "H4-1BB"
?       OTHER INFORMATION: /number= 1
PCT-US96-03965-7

Query Match      100.0%; Score 838; DB 6; Length 838;
Best Local Similarity 100.0%; Pred. No. 9.7e-251;
Matches 838; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aatcaagcttctagatcatcaccctgtgccaagattcatcatcaggaaacagctgttcaaa 60
   |||||
Db 1 AATCAGCTTTGCTAGTATCATCTGTCGCCAGATTTCATGGAACACGCTTTTCAAA 60

QY 61 catagtagcacctctgtctgtcctcaacttgaggagacaagatcatgccaagctcc 120
   |||||
Db 61 CATAGTAGCCACTCTGTGCTGGCTCAACTTTGAGAGACAAAGATCATTTGCAGATGCC 120

QY 121 tttagtaactgcccagctgtgatactctgtgataataacaagaaatagatttgcattcc 180
   |||||
Db 121 TTGAGTAAGTACGCCACCTGATCATTTCTGATTAATACAGGAAATGAGATTGCCATGCC 180

QY 181 ctgtccctcaaatagttctccacagcaggctgagacaagagacctgtacatatgagca 240
   |||||
Db 181 CTGTCCCTCAAAATAGTTCTCCAGCGCAGAGTGACAAAGACCTGTACATATGCAGACA 240

QY 241 gtttaagaagtgttcttcaagaccaggaagagtgcttccctcacaagcaatgcaagtgta 300
   |||||
Db 241 GTTAAAGGTGTTTTCAGGACCAAGAGGAGTGTCTCCACACGCAATGCAGAGTGTGA 300

QY 301 ctgcacctccaggggtttcactgctgggggagagatgtagcatgtgtgaaagaattgtaa 360
   |||||
Db 301 CTGCACCTCCAGGGGTTTACTGCTGGGGGACGATGTCAGATGTGTAACAGGATTTGTA 360

QY 361 acaaggtcacaagactgacaataaaaggctgtgaaagactgtgcttcttggaacattaaaga 420
   |||||
Db 361 ACAAGGTCAAGAACTGACAAAAAAGGTGTGTAAGACTGTGCTTTGGGACATTAAACA 420

QY 421 tcsagaacgtgtgacatctgtgcaccctgtgacaacactgttcttggatgaaagtctgtc 480
   |||||
Db 421 TCAGAAACGTGGCATCTGTGCACCTGTGACAAACTGTTCTTTGGATGAAAGTGTGCT 480

QY 481 tgtgaatggagaaagagagagagagagagagagagagagagagagagagagagagagag 540
   |||||
Db 481 TGTGAATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540

QY 541 gggagacatccctctgtgaccccgctgcccctgcaagagagacaagacacctccagagat 600
   |||||
Db 541 GGGAGACATCCTCTGTGACCCCGCTGCCCTTCGACAGAGACACGACACTCTCGCGAGAT 600

QY 601 catctcccttcttctgtgagctgagcagtcgactgcgtgtcttctcctgtcttctcctcac 660
   |||||
Db 601 CATCTCCCTTCTTCTGTGAGCTGAGCTGACGTCGACTGCGTTCTCTCTGCTGTCTTCCTC 660

QY 661 gctcgcgttctctgtgtgttaaacgaggagacaagaagaacctcgtatataatcaacaac 720
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Db 661 GCTCGGTTCTCTGTTGTTAAACGGGCGAAGAAACTCCTGTATATTCAAAACACC 720
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QY 721 attatgagaccagtagacaactactcaagagaaagatgctgtgactgcccattccaga 780
|||||
Db 721 ATTATGAGACCAGTAGACAACACTACTCAAGAGAAAGATGCTGTACTGCCATTTCCAGA 780

QY 781 agaagaagaagagagatgtgaactgtgaaatgaaatgaatgaatgaatgaatgaatgaat 838
|||||
Db 781 AGAAGAAGAAGAGAGATGTGAATGTGAATGTGAATGTGAATGTGAATGTGAATGTGA 838

RESULT 3
US-08-236-918A-7
Sequence 7, Application US/08236918A
Patent No. 5674704
GENERAL INFORMATION:
APPLICANT: Alderson, Mark R.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple 7.5.3
SOFTWARE: Microsoft Word, Version #6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,918A
FILING DATE: 06-May-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/060,843
FILING DATE: 07-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2801-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1415 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: hu4-1BB
FEATURE:
NAME/KEY: CDS
LOCATION: 120..887
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 189..884
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 120..188
US-08-236-918A-7

Query Match      99.8%; Score 836.4; DB 1; Length 1415;
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Best Local Similarity 99.9%; Pred. No. 4e-250;
Matches 837; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 aatcagcttctgcatcatatcaccgttccagattctcattcaggaacagctgttaca 60
Db 80 AATCAGCTTCTGCTATCATCATCTGCTCCAGATTTCATCAGGAAACAGCTGTACAA 139
QY 61 catagtaacacactgttctgctcactcactttagaggaacaatcatcacaatcc 120
Db 140 CATAGTACCACTGCTGTGCTGCTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 199
QY 121 ttgtagtaactgtccagctgtgtacattctgtgataataacaggaatcagatttgc 180
Db 200 TTGTAGTAACTGCCAGCTGTGATCTGTGATTAATTAACAGGATTCAGATTGCACTCC 259
QY 181 ctgtccctcaaatagtttctcagcagcaggtgtgacaagaagactgtgacatgtcag 240
Db 260 CTGTCTCTCAATATATTTCTCCAGCGAGGTGACAAAGACCTGTGACATGTGACAGCA 319
QY 241 gtgtaaaggttcttcagagaccagaagaaggtgtctcctccacacagcaatgtcag 300
Db 320 GTGTAAAGTGTTCAGAGACCGAGAGAGAGTGTCTCCACACAGCATGCAAGTGTCA 379
QY 301 ctgcactcagaggttctcactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 360
Db 380 CTGCACCTCCAGGGTTCCTGCTGCGGGGAGAGATGACAGCATGTGTGAACAGATTGTAA 439
QY 361 acaaggtcaagaactgacaaaaaaggtgtgtaaaagactgtgtgtgtgtgtgtgtgt 420
Db 440 ACAAGGTCAAGAACTGACAAAAAAGTGTGTAAGACTGTGTGTGTGTGTGTGTGTGTGT 499
QY 421 tcagaaacgtgtcactgttcgacctgtgacaaactgttcttctgtgtgtgtgtgtgt 480
Db 500 TCAGAAAGTGTGGCATCTGTGACACCTGTGACAAACTGTCTTGTGATGGAATGTGTGT 559
QY 481 tctgaatgtgacgaagaagaagaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 540
Db 560 TGTGAATGGGAGAGAGAGAGAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 619
QY 541 gggagacatcctctgtgacacccgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 600
Db 620 GGGACATCTCTGTGTGACCCCGCTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 679
QY 601 catcctccttcttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 660
Db 680 CATCTCTCTTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 739
QY 661 gctccgttcttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 720
Db 740 GCTCCGTTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 799
QY 721 attatagacagcagtaacaaactcaagaagagaatgtgtgtgtgtgtgtgtgtgt 780
Db 800 ATTATGTGACCACTGTAACAACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 859
QY 781 agaagaagaagaagatgtgaactgtgaatgtgaagtcataatgaggtgtgtgtgt 838
Db 860 AGAAGAAGAAGAGAGATGTGAATCTGAATGAATGAATGAATGAATGAATGAATGA 917
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RESULT 4
US-08-816-605-1
Sequence 1, Application US/08816605
Patent No. 5874240

GENERAL INFORMATION:
APPLICANT: NI, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Gentz, Reiner
TITLE OF INVENTION: Human 4-1BB Receptor Splicing Variant
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue

```
/? CITY: Rockville
/? STATE: MD
/? COUNTRY: USA
/? ZIP: 20850
/? COMPUTER READABLE FORM:
/? MEDIUM TYPE: Floppy disk
/? OPERATING SYSTEM: PC-DOS/MS-DOS
/? SOFTWARE: Patent Release #1.0, Version #1.30
/? CURRENT APPLICATION DATA: US/08/816, 605
/? APPLICATION NUMBER: 36, 373
/? FILING DATE: 13-MAR-1997
/? CLASSIFICATION: 435
/? ATTORNEY/AGENT INFORMATION:
/? NAME: Brookes, A. Anders
/? REGISTRATION NUMBER: PF254
/? TELECOMMUNICATION INFORMATION:
/? TELEPHONE: 301-309-8512
/? TELEFAX: 301-309-8504
/? INFORMATION FOR SEQ ID NO: 1:
/? SEQUENCE CHARACTERISTICS:
/? LENGTH: 946 base pairs
/? TYPE: nucleic acid
/? STRANDEDNESS: single
/? TOPOLOGY: linear
/? MOLECULE TYPE: DNA (genomic)
/? FEATURE:
/? NAME/KEY: CDS
/? LOCATION: 124..780
/? FEATURE:
/? NAME/KEY: sig_peptide
/? LOCATION: 124..177
/? FEATURE:
/? NAME/KEY: mat_peptide
/? LOCATION: 178..780
/? US-08-816-605-1
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Query Match 72.6%; Score 608.8; DB 3; Length 946;
Best Local Similarity 86.9%; Pred. No. 1.5e-175;
Matches 728; Conservative 0; Mismatches 2; Indels 108; Gaps 1;

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QY 1 aatcagcttctgcatcatatcaccgttccagattctcattcaggaacagctgttaca 60
Db 84 AATCAGCTTCTGCTATCATCATCTGCTCCAGATTTCATCAGGAAACAGCTGTACAA 143
QY 61 catagtaacacactgttctgctcactcactttagaggaacaatcatcacaatcc 120
Db 144 CATAGTACCACTGCTGTGCTGCTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 203
QY 121 ttgtagtaactgtccagctgtgtacattctgtgataataacaggaatcagatttgc 180
Db 204 TTGTAGTAACTGCCAGCT----- 222
QY 181 ctgtccctcaaatagtttctcagcagcaggtgtgacaagaagactgtgacatgtcag 240
Db 223 ----- 222
QY 241 gtgtaaaggttcttcagagaccagaagaaggtgttctccaccacgaatgtcaggtgt 300
Db 223 -----GCTGTTTTCAGAGACCGAGAGAGAGTGTCTCCACACAGCAATGCAAGTGTGA 275
QY 301 ctgcactcagaggttctcactgtcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 360
Db 276 CTGCACCTCCAGGGTTCCTGCTGCGGGGAGAGATGACATGTGTGAACAGATTGTAA 335
QY 361 acaaggtcaagaactgacaaaaaaggtgtgtaaaagactgttcttgggacatttaaga 420
Db 336 ACAAGGTCAAGAACTGACAAAAAAGTGTGAAGACTGTGTGTGTGTGTGTGTGTGTGT 395
QY 421 tcagaaacgtgtcactgttcgacctgtgacaactgttcttggatgtgaaatctgtgt 480
Db ----- 480
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?	LENGTH: 2347 base pairs
?	TYPE: nucleic acid
?	STRANDEDNESS: single
?	TOPOLOGY: linear
?	MOLECULE TYPE: cDNA to mRNA
?	ORIGINAL SOURCE: murine
?	ORGANISM: murine 4-11B
?	FEATURE:
?	NAME/KEY: CDS
?	LOCATION: 146..916
?	FEATURE:
?	NAME/KEY: mat_peptide
?	LOCATION: 146..913
?	PUBLICATION INFORMATION:
?	AUTHORS: Kwon, Byoung Se
?	AUTHORS: et al.,
?	TITLE: cDNA sequences of two inducible T-cell genes
?	JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
?	VOLUME: 86
?	ISSUE: March
?	PAGES: 1963-1967
?	DATE: 1989
?	RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 2347
?	PCT-US96-03965-1

Query Match	40.5%	Score 339.2	DB 6	Length 2347
Best Local Similarity	67.8%	Pred. No. 1.3e-95		
Matches 537	Conservative 0	Mismatches 243	Indels 12	Gaps

QY	14	agatcatcactctgtgccagatattcatatggaagacagctgttaacacatagtagccact	73
DB	119	AGGTGCTCGTGCATGTGACATTTGGCCATGGGAAACAACCTGTTACACAGTGGTGCATT	178
QY	74	ctgtgtctgtgtccctcaactttagagagacaaagatcatctgtcagagtcctcttgaatactgc	133
DB	179	GTCCTGCTGCTAGTGTGGCTGTGAGAAAGGTGGAGCCGTGCAGAACTCTTGATTAAGT	233
QY	134	ccagctgtgtacatctctgtataataacagagaatcagatcttcagtcctctcccaat	193
DB	239	CAGCTGTGACTTTCTGACAGAAATATAC--AATCCAGTCTGCAGAGAGCTGCCCTCAAGT	293
QY	194	agttctccagcgcaggtgtgacaaagaacactctgtacatatgacagcagtgtaagtgctt	253
DB	296	ACCTTCTCCACCAATAGGTGGACACCCGAACTGTAACTCTCAAGATGTGTGCAGGCTAT	353
QY	254	ttcagagaccagaaagagtgcttctccacacagcaatgcagagtgtagtcaaccacagg	313
DB	356	TTTCAGGTTCAAGAAAGTTTGCTCCTTACCCACAAACGGGAGTGTGAGTGCATTGAAGA	413
QY	314	tttactgtcctgtgggcaagatgacagcatgtgtgaacagatgtglaaacaagttcaagaa	373
DB	416	TTTCATTGCTTGGGGCCACAGTGCACACGATGTAAAAAGGACTCAGGCTCGCCAGAG	473
QY	374	ctgcaaaaaaaggctgttaagactgttgcctttgggacatttaacgatcagaagc---t	433
DB	476	CTAACGAGACGGGTGTGCAAACTGTAGCTGTGGAACTTTTAATGACCAACAGCTACT	533
QY	431	ggacatctgtcagacccttgacaacactgttctcttgaatggaagtcctgtcgttgaatgg	490
DB	536	GCGCTGTGTGACCTGTGACGAACTGCTCTTAGCGGAAGTGTGTGCTTAAGACGGGG	590
QY	491	acgaagaagagagacgtgtgtctgtgtgaaacatctccagctgaacctctctccggagacatc	550
DB	596	ACCAAGGAGAGACGTGTGTGTGGACCCCTGTGTGACACTTCTCTCCAG--TACC	653
QY	551	tctgtgaccccgctgcgccctgcagagagacaggaacactctcgagatcatctcttc	610
DB	653	ACCAATTTCTGTGATCTCCAGAGGAGAGACAGAGAGGACACTCTTGACAGTCTTAAGT	710
QY	611	ttctgtgcgtgacgtcagactcgtgtccttctcgttctctctcctcaacgtccgttcc	670
DB	713	TTTCCTGGCGCTGACATG---GCTTTCCTGTGTGACCCCTGATCTTCAATTAAGTCTGTG	765

Qy	671	tcctctttaaaccgggacagaagaanaactccgtgatatatcaacaacacattataga	730
Db	770	tctgtgcctcaatgatgacagaaaaaaattccccacacattatcagcaacacatttaaaag	829
Qy	731	ccagtaacaaactactacagagaagaatgctgctgtatgctgcgaatttcaagaagaagaagaa	790
Db	830	accactggagcagcgtccaaagagaagatgcttggtagctgcccattotccacagaaagaagaa	889
Qy	791	ggagagatgtgaa	802
Db	880	ggagcagcagcagga	901

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RESULT 6
US-08-236-918A-5
: Sequence 5, Application US/08236918A
Patent No. 5674704
GENERAL INFORMATION:
: APPLICANT: Alderson, Mark R.
: APPLICANT: Goodwin, Raymond G.
: APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
: ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
: City: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple 7.5.3
SOFTWARE: Microsoft Word, Version #6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,918A
FILING DATE: 06-May-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/060,843
FILING DATE: 07-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2801-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ. ID NO.: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 768 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: mu4-1BB
FEATURE:
NAME/KEY: CDS
LOCATION: 1..768
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 70..768
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1..69
US-08-236-918A-5

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Query Match	39.5%;	Score 331.4;	DB 1;	Length 768;
Best Local Similarity	-68.2%;	Pred. No. 1.9e-93;		
Matches 522;	Conservative	0;	Mismatches 231;	Indels 12;
				Gaps 4;

OY	41	atgggaacaacgctgttacaacatagtagcaacctgtgttcggtgcctcaactttgag	100
Db	1	ATGGGAACAACACTGTTTACAACGTGCTGTCTATTGTGCTGCTGCTAGTGGCCTGTGAAG	60
OY	101	acaagatcatctgcaggatcctctttagtaactgcccagcttgatcatctctgataataac	160
Db	61	GMGGAGCCGTCGACAAACTCCTGTGATTAACGTACGCGCTGGTACTTCTGCAAAAATAC	120
OY	161	aggatcagatlttgcagtccctgtccctccaatagtltctcagcgcaagtggacaag	220
Db	121	--AATCCAGTCGTGCAMAGGTGCCCTCCACAACTTCCTTCACCAATAGGTCACACCG	177
OY	221	acctgtgcacatagcagcgagtfaaaggtgttttcagagccaggaaagagttctcc	280
Db	178	AACTGTAACTATCTGCAGAGTGTGTGCAGGCTATTTCAGAGTTCAAGAAAGTTTGCTCTCT	237
OY	281	accagcaatgcagaagtgtagctgactccagaggttcaactgctccggtggcagaatgcag	340
Db	238	ACCACAACGGGGAGGTGTGATGCAATTGAAGATTCCATTGCTTGGGGCCACAGTGACC	297
OY	341	atgtgtgcacaggaatgtgtaaacaaagttcaagaactgcacaaaaaagttgtaaagactgt	400
Db	298	AGATGTGAAAAGAGACTGCAGGCGCTGGCCACGAGAGCTAAAGCAGGGGTCCAAAACCTGT	357
OY	401	tgctctgggaacttaagaatcacaagaag---tgacatctgtgacacctgtgacaaactgt	457
Db	358	AGCTTGGGAACCTTTAAAGACCAAGACGTAAGTGGCGTGTGTCAACCTGTGGACAACCTGC	417
OY	458	tctttggaatggaaagctctgtctgtgtgtaatggaacgaaggaaggaacgtgtctgtgga	517
Db	418	TCTTAAAGCGGAAGGTGTGTGCTTTAAAGCCGGGACCAAGGAGAAAGACGTGTGTGTGGA	477
OY	518	ccatctccagctgacctctctccgggagacatcctctgtgacccgcgtgccctgtgaga	577
Db	478	CCCCCTGTGGTAGCTTCTCCACAG---TACCACCACTTTCTGTGACTCCAGAGGAGGA	534
OY	578	gagcaggaagaacatccgcagacatcatctctcttctttgttgcgctgagctgacgtgcgt	637
Db	535	CCAGAGAGGGCACTCCTTGACAGGTCTCTTAACCTTGTTCTGTGGGCGCTGAATCG--GCTTTG	592
OY	638	ctcttcctgcgtcttctccacagctccgcttctctgtgtgttaaagcgggcagaaaga	697
Db	592	CTGCTGGCGCCGTGATCTTATTAAGTCTCTGTCTGTCTGTGCTCAAAATGATCAGGAAAAA	651
OY	698	ctctcgtatataatcaacaacacttaatgagaccagtaacaaactactcaagaggaat	757
Db	652	TTCCCCCAATATTCACAAACCACTTTTAAGAAAGCACACTGAGCAGCTCTCAAGAGGAAGAT	711
OY	758	ggctgtagctcgcgaattccagaagaagaagaagaagatgtgta 802	
Db	712	GCTTTAGCTGCTCCAGTGTCCACAGGAAGAAAGAGAGAGAGGA 756	

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COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ. ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZgpt-F15
US-08-232-463-14
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Query Match          5.4%; Score 45.6; DB 1; Length 7218;
Best Local Similarity 10.0%; Pred. No. 0.00033;
Matches 21; Conservative 115; Mismatches 74; Indels 0; Gaps 0;

QY 470 aagctcgtctgtgaatgagcaagagagagagctgtctgtgacatccagct 529
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1029 AATTCGACCTTGCTGCGAGGCGAGGAGCTTGCATYYYYYYYYYYYYYYYY 1088

QY 530 gacccctccgagagcattctgtgacccgcctgcccctgagagagccagacac 589
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1089 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1148

QY 590 tctccgagatcatctctcttctctgctgagctgacgtcgctctctcctgctg 649
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1149 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1208

QY 650 tctctccacgctccgctctctctgtgt 679
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1209 YYYYYYYYYYYYYYYYYYYYYYYYYYYY 1238

RESULT 8
US-08-232-463-14/C
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ. ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZgpt-F15
US-08-232-463-14
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Query Match          5.0%; Score 42.2; DB 1; Length 7218;
Best Local Similarity 2.4%; Pred. No. 0.0037;
Matches 8; Conservative 188; Mismatches 131; Indels 0; Gaps 0;

QY 203 agcgcaagtgagacaagagcctgtgacatagcagcagtgtaagtgcttcagagcc 262
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1383 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1324

QY 263 aggaagagtgctccccaagcaatgagagtgagcagcctcagaggttcactg 322
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1323 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1364

QY 323 ctgggggcaagatgacgcatgttgacaagatgttaaacaggtcaagacgtacaaa 382
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DB 1263 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1204

QY 383 aaagttgtaagactgtcttgagacattaaacgatacagaacgtggcatctgca 442
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1203 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1144

QY 443 ccttgacaacactgtcttgatgagaagctgtgctgtgtaatggagagagagag 502
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1143 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1084

QY 503 gacgtgctgtgacatccagct 529
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DB 1083 RRRRRRRRRRRRRRRRRATCGCAAGCT 1057

RESULT 9
US-08-162-809-1
; Sequence 1, Application US/08162809
; Patent No. 5457048
; GENERAL INFORMATION:
; APPLICANT: Pasquale, Elena B.
; APPLICANT: Sajjadi, Fereydon G.
; TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
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      MEDIUM TYPE: Floppy disk
      COMPUTER: Apple Power Macintosh
      OPERATING SYSTEM: Apple Operating System 7.5.5
      SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
      CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/996,139
        FILING DATE: 22 DECEMBER 1997
      CLASSIFICATION:
        PRIOR APPLICATION DATA:
          APPLICATION NUMBER: USSN 60/064,671
          FILING DATE: 14 OCTOBER 1997
        PRIOR APPLICATION DATA:
          APPLICATION NUMBER: USSN 08/813,509
          FILING DATE: 07 MARCH 1997
        PRIOR APPLICATION DATA:
          APPLICATION NUMBER: USSN 08/772,330
          FILING DATE: 23 DECEMBER 1996
      ATTORNEY/AGENT INFORMATION:
        NAME: Perkins, Patricia Anne
        REGISTRATION NUMBER: 34,693
        REFERENCE/DOCKET NUMBER: 2851-A
      TELECOMMUNICATION INFORMATION:
        TELEPHONE: (206)587-0430
        TELEFAX: (206)235-0644
      INFORMATION FOR SEQ ID NO: 5:
      SEQUENCE CHARACTERISTICS:
        LENGTH: 3136 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
      MOLECULE TYPE: cDNA
      HYPOTHETICAL: NO
      ANTI-SENSE: NO
      ORIGINAL SOURCE:
        ORGANISM: HOMO SAPIENS
      IMMEDIATE SOURCE:
        LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS
      CLONE: FULL LENGTH RANK
      FEATURE:
        NAME/KEY: CDS
        LOCATION: 39..1886
      US-08-996-139-5

Query Match          4.2%; Score 34.8; DB 5; Length 3136;
Best Local Similarity 60.6%; Pred. No. 0.49;
Matches 57; Conservative 0; Mismatches 37; Indels 0; Gaps 0

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    || || || || || || || || || || || || || || || || || || || ||
Db 537 GACAATTCACACCCCTGGACCAACGTACCTTCCTGGAAAGAGTAGAACATCATGG 596

QY 491 acgaagagagagagcgtgtgtctgtgacacatc 524
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Db 597 ACAGAGAATCCGATGCGCTTGCAGTCTTCTC 630

RESULT 13
US-08-911-423-5
; Sequence 5, Application US/08911423
; Patent No. 611090
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Zlocnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California

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Fri Nov 24 17:29:10 2000

us-08-955-572-1.rni

Page 11

Db 38794 gcactcgtatctactccttcttcttaagac 38822

Search completed: November 22, 2000, 05:34:18
Job time: 17078 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 22, 2000, 00:29:20 ; Search time 770.21 Seconds

(without alignments)
6726.986 Million cell updates/sec

Title: US-08-955-572-1

Perfect score: 838
Sequence: 1 aatcagcttgctagtatca.....aataggcctgtggacttt 838

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7189864 segs, 3091403243 residues

-Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

-Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	491	58.6	570	34	BE207340	BE207340 ba85f11.y
2	272	32.5	548	34	BE233113	BE233113 139153 MA
3	241	28.8	630	1	AA109726	AA109726 mp10f11.r
4	235.2	28.1	667	9	AI236084	AI236084 EST232646
5	231	27.6	674	7	AA946462	AA946462 EST201961
6	203.2	24.2	589	1	AA087107	AA087107 mol3901.r
7	198.6	23.7	491	12	AI664286	AI664286 ue83005.r
8	79.8	9.5	332	9	AI172529	AI172529 UT-R-C2P-
9	58.6	7.0	330	25	AW920027	AW920027 EST35131
10	57.4	6.8	291	11	AI555584	AI555584 UT-R-C2P-
11	42.4	5.1	688	2	AA166859	AA166859 zq41c02.s
12	40.2	4.8	578	5	AA618624	AA618624 np38h10.s
13	39.8	4.7	529	38	N80901	N80901 zb07b08.s1
14	38.8	4.6	304	29	BB290438	BB290438 BB290438
15	38	4.5	468	104	AA0933474	AA0933474 RPT-23-2
16	38	4.5	573	106	AA0205913	AA0205913 RPT-23-3
17	37.8	4.5	748	109	A2228414	A2228414 RPT-23-7
18	37.6	4.5	383	88	AA072028	AA072028 HS_3020.A
19	36.6	4.4	803	112	CNS018FX	AI109287 Drosophill
20	36.2	4.3	404	24	AW746620	AW746620 WSL_54_F0
21	36.2	4.3	442	6	AA775053	AA775053 ac76103.s
22	36	4.3	751	103	AA0869200	AA0869200 nbe00341
23	36	4.3	1101	112	CNS01784	AL107710 Drosophill
24	35.8	4.3	382	24	AA796144	AA796144 MR2-UM002
25	35.8	4.3	676	109	A2276416	A2276416 RPT-23-1
26	35.6	4.2	291	28	BB232607	BB232607 BB232607
27	35.6	4.2	430	36	BE524618	BE524618 NS2B9STM
28	35.4	4.2	904	108	A2208857	A2208857 SP_0152.A
29	35.4	4.2	1068	115	CNS0509F	AL148972 Tetraodon
30	35.2	4.2	417	20	AW146746	AW146746 614083B05
31	35.2	4.2	504	102	AA0785579	AA0785579 HS_3077.A
32	35	4.2	375	20	AW157881	AW157881 D5 Neosp
33	35	4.2	459	114	CNS0361Q	AL242423 Tetraodon
34	35	4.2	1101	112	CNS012RM	AL101932 Drosophill
35	35	4.2	1101	112	CNS016N6	AL106956 Drosophill
36	35	4.2	1201	112	CNS01638	AL106228 Drosophill
37	34.8	4.2	261	29	BB324451	BB324451 BB324451
38	34.8	4.2	424	90	AA0218065	AA0218065 HS_3251.B
39	34.8	4.2	561	21	AA391329	AA391329 QV0-ST021
40	34.8	4.2	562	21	AA380345	AA380345 QV3-HT026
41	34.6	4.2	751	108	A2200704	A2200704 SP_1026.A
42	34.6	4.1	505	5	AA613256	AA613256 no19h02.s
43	34.6	4.1	679	102	AA0795961	AA0795961 nbx000587
44	34.6	4.1	1101	112	CNS006BP	AL064052 Drosophill
45	34.4	4.1	287	3	AA310664	AA310664 EST181611

ALIGNMENTS

RESULT 1
BE207340

LOCUS	BE207340	570 bp	mRNA	EST	27-JUN-2000
DEFINITION	ba85f11.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2924109 5' similar to gb:j04492 Mouse T-cell receptor 4-1BB protein mRNA, complete cds (mouse), mRNA sequence.				
ACCESSION	BE207340				
VERSION	BE207340.1	GI:8750738			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 570)				
ADDITIONAL	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling Hong/Rubin Laboratory DNA Sequencing by: The I.M.A.G.E. Consortium (LNLN) Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/HLN at: Image.lnl.gov/image/html/lresources.shtml Seq primer: -40RP from Gldco High quality sequence stop: 516.				
FEATURES	location/Qualifiers				
SOURCE	1..570				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/clone="IMAGE:2924109"				
	/clone_lib="NIH_MGC_14"				
	/tissue_type="renal cell adenocarcinoma"				
	/lab_host="DH10B (phage-resistant)"				
	/note="Organ: kidney; Vector: pOT7; Site:1. XhoI; Site:2. EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."				
BASE COUNT	157 a	117 c	145 g	151 t	
ORIGIN	157 a				
	117 c				
	145 g				
	151 t				
Query Match	58.6%; Score 491; DB 34; Length 570;				
Best Local Similarity	100.0%; Pred. No. 4.3e-134;				
Matches	491;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;		
	1 aatcagcttcctgatacatcattcgtccagatttcataatgggaacagctgttaca 60				
	80 AATCAGCTTCTGATATCATATCTGTCAGATTTCATGGAACAGCTGTTCACA 139				
	61 catagtaaccactctgtctcgtgtcccaactttgagaggaacaagatcagagatcc 120				
	140 CATAGTACCACCTGTCGTCGTCCTCACTTTCAGAGCAACATCATTCAGAGATCC 199				
	121 ttgtagtaactcgtccagctgtgtacattctgtgataataacaggaatcagatttcagtc 180				
	200 TTGTGTGTAACCTGCCAGCTGTACATCTGTGATTAATTAACAGATTCAGATTTCAGATCC 259				
	181 ctgtcttcctcaaatgcttcctcagagcagtgagaaagagcctgtgacatagagca 240				
	260 CTGTCTCTCAATATGTTTCTCCAGCGAGGTGGAAGAAAGACCTGTGACATATGAGGCA 319				
	241 gtgtaaagtgctttcagagcaggaagagtgctccaccacagcaatgcagagtgta 300				
	320 GTGTAAAGTGCTTTTCAGAGCAGGAGAGAGTGTTCTCCACACCAATGCAAGTGTGA 379				
	301 ctgcaactcagagtgctcactcgtgtgggcagagatgcagcatgtgtgacagagatgttaa 360				

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Db 380 CTGCACATCCAGGGTTTCACTGCTGGGGGAGAGATCAGCATGHTGACAGATGTAA 439
Qy 361 acaaggtcaagaactgcacaaaaaagtttaagaactgtgtcttgggacatttaaca 420
Db 440 ACAAGGCAAGAACTGCAAAAAAGGTTGTAAGACTGTGCTTGGGACATTAAAGA 499
Qy 421 tcgaagaacgtgagactgtgtgacacctgtgacaaactgtcttggatggaagactgtgct 480
Db 500 TCAGAAACGTCGCACTGTGTGACCTGTGACAACTGTTCTTGGATGGAAGTCTGTGCT 559
Qy 481 tctgaatggga 491
Db 560 TGTGAATGGGA 570

RESULT 2
LOCUS BE233113 548 bp mRNA EST 10-JUL-2000
DEFINITION BE233113 139153 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BE233113
VERSION BE233113.1 GI:9017831
KEYWORDS EST.
SOURCE Sus scrofa
ORGANISM pig.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
1 (bases 1 to 548)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keele,J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross_match with the -m1nscore 18
and -mismatch 12 options.
PCR primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCACGACG
Plate: 75 row: P column: 5
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
1.548
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1P1G"
/tissue_type="pooled"
/lab_host="DH10B"
/note="vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT 138 a 125 c 162 g 123 t
ORIGIN
Query Match 32.5%; Score 272; DB 34; Length 548;
Best Local Similarity 73.6%; Pred. No. 2e-69;
Matches 381; Conservative 0; Mismatches 95; Indels 42; Gaps 1;

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Qy 431 ggcatctgtgacctggacaaactgtcttttggatggaagctgtgttgatggg 490
Db 158 GGCTCTGTGCACCTCTGCAGGAGACTGTTCTTGGCTGGAAAGCCTGCTCATATAAGGG 217
Qy 491 acgaagagagagagcgtgtgtgtgtgacacatctcagctgacacctctcggagacatcc 550
Db 218 ACGAAGCAGAGAGACGTGTGTGTGTGACCAAGGCCAAGGACTTCTCT----- 265
Qy 551 tctgtgaccccgctgccctcgagagagccagaaactctccagatcatctctc 610
Db 266 -----CCAGGTCACACTTCCTCCATGTCATCATCTTC 295
Qy 611 ttcttcgctgaagctgactgctgtctctctctctgtctctctcccaagctgttc 670
Db 296 TTTCTGTCACTGATGATCACTGCTGCTTGTCTCTGATCTCTACCTGCGCTCCGTTTC 355
Qy 671 tctgtgttaacggcgagaaagaactctgtatattatcaaaacacattatgaga 730
Db 356 TCTGTTTTCACAGGCGCAGAGAAACTCTGTATATAGTCANACACCTTCTGAG 415
Qy 731 ccagtaacactactcaagaagagatgctgtagctgcgcgattccagaagaagaa 790
Db 416 CCAGCGCAACGGTCCAAAGAGAGATGCGTGCAGCTGCGGTTTCCAGAAAGAGAGAA 475
Qy 791 ggagatgtgaactgtgaatggaatgcaatagagctg 828
Db 476 GCGCAGTGTGAACATCATCGAAATCCAGAGAGATG 513

RESULT 3
LOCUS AA109726 610 bp mRNA EST 02-OCT-1997
DEFINITION mp10f11.r1 Life Tech mouse embryo 8 5dpc 10664019 Mus musculus cDNA
clone IMAGE:568845 5' similar to gb:J04492 Mouse T-cell receptor
4-11B protein mRNA, complete cds (mouse);, mRNA sequence.
ACCESSION AA109726
VERSION AA109726.1 GI:1661789
KEYWORDS EST.
SOURCE Mus musculus.
ORGANISM house mouse.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
1 (bases 1 to 610)
REFERENCE
AUTHORS
Marrin,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,B.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI: 343493
Seq primer: -28M13 rev1 from Amersham
High quality sequence stop: 399.
Location/Qualifiers
1.610
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="IMAGE:568845"
/clone_lib="Life Tech mouse embryo 8 5dpc 10664019"
/tissue_type="embryo"
/dev_stage="8 5dpc embryos"
/lab_host="DH10B"
/note="Organ: whole embryo; Vector: pCMV-SPORT2; Site_1:

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BASE COUNT	ORIGIN	
139 a	SalI; Site-2: NotI; Cloned unidirectionally. Primer Oligo dT. 8-5dpc embryos. pCMV-SPORT2 vector."	150 t
146 c		175 g

The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208

Query Match	28.8%	Score 241	DB 1	Length 610
Best Local Similarity	67.7%	Pred. No. 2.9e-60		
Matches 369	Conservative 0	Mismatches 170	Indels 6	Gaps 2

QY	13	tagtatactactgctggcaggaattcatcaatgggaagaacagctgtttcaacaatagtagccac	72
Db	55	TGGTCTCCTGTGCATGTGTACATTTTGGCCATGGGGAACACCTTTACAAAGTGGTGCTAT	114
QY	73	tctgttgtctgttccctaactttgagaggaacaagaatcatctgtcaggaatcccttgttaactcy	132
Db	115	TGTGCTGGCTGATAGTGGGCTGTGAGAAAGGTGGAGCCCGTGCAGAACTCCTGTGTATACAG	174
QY	133	cccagctggttatactctgtatataataacaagaatcagaattgtcagtcacctgtccctccaaa	192
Db	175	TCAGCCTGTGATCTTCTCGAGAAATATAC--AATCCAGTCTGCAAGAGCTGCGCTTCCAAAG	231
QY	193	tagttttccacgcgaggttggacaagaagacctgtacatcatcaagcagtgtaaaagtggt	252
Db	232	TACCTTCTCCACATATAGGTGGAGACCCGACACTGTATACATCTCGAGTGTGTGGACGGCTA	291
QY	253	tttcaagaaccagaaggaagtgtctctccacccaagaatgtcagaagtgtgactgtcacctcag	312
Db	292	TTTTCAGGTTCAAAGAGTTTGTGCTCCTCTATCCACCAAAAGCGAGTGTGATGTGATTTGAAG	351
QY	313	gtttactatgctctgggggacaagaatgcagcaatgtgtgaaacaagaattgtaaaagaattca	372
Db	352	ATTCCATTGCTTGGGGCCACACAGTGCACCAAGATGTAAAAAGGACTCGACGCTCGGCCAGGA	411
QY	373	actggcaaaaaaaggtttlaaagactgtgtgtgtttgttggacaattaaacgatcagaagaacg---	429
Db	412	GCTTAACGAAGCAGGGTTTGCATAACCTGTATAGCTTGGGAACATTTAATAGCAACACGGTAC	471
QY	430	tggcaatctgtcgaacctgtgacaacactgttcttttgatgagaaagtctgttctgttgaatg	489
Db	472	TGGCGTGTGTGACACCTGTGACCAACTGTGCTCTAGACGGAAGTGTGTCTTAAAGACGG	531
QY	480	gaacgaagaagaaggaagctgtgtctgtgacacatcccaagtcaactctctccgggaacac	549
Db	532	GACCAACGGAAGAAGACGTGTGTGTGTGACCCGCTGTGTGAGCTTTCTCCAGTACACCATTT	591
QY	550	ctcttg 554	
Db	592	cttg 596	

FEATURES	SOURCE	Location/Qualifiers
		1..687
		/organism="Rattus sp."
		/db_xref="ATCC (inhost):2042770"
		/db_xref="taxon:10118"
		/clone="ROVDB21"
		/clone_1lb="Normalized rat ovary, Bento Soares"
		/note="Organ: ovary; Vector: pT7n3Pac; Site_1: EcoRI Site_2: NotI"
BASE COUNT		149 a 189 c 180 g 169 t
ORIGIN		

Query Match	28.1%;	Score 235.2;	DB 9;	Length 687;
Best Local Similarity	67.6%;	Pred. No. 1.5e-58;		
Matches 346;	Conservative 0;	Mismatches 163;	Indels 3;	Gaps 1

QY	294	atgtagctgaacccccaaggtttcaactctgcgtggggcaggatgcagcatglttgaaacg	353
Db	687	AGTGTAAAGTGGCTGAAGGGATTCCACTGCTTTGGGCCAAAGTGTACCAAGTGTGAAGG	628
QY	354	attgttaaaccaagytcaagaactgcagcaaaaaaaggtgttaagaactglttccttggaacat	413
Db	627	ACTGCAAGGCCCGCGCCAGGAACTTAACGGACAGAGGTTGTATAAACTGTGGCTTGGGAACGT	568
QY	414	ttaacgacatcaagaacg---tggcatctgtcgacccctgcagcaaacgtgtccttggatbysaa	470
Db	567	TTAATGACACAGACAGCGCGCGCGCTGTGCGCCAGCCCTGGACGAACGTCTCTAAGACGAA	508
QY	471	agctcgtgctctgtgtaattggagaagggagggaaagctgctgtctgtgacatctccagctg	530
Db	507	GGTCTGTGCTTTAAGATATGGGACCAAGGAAAGACGTGTCTGTGTGACCCCTCTGTGTC	448
QY	531	acctctcccggaagcatcctctctgaccccgccctgcagcccttcgagaagagcagaacact	590
Db	447	GCCTTCTTCCCAAGTACCCACTCTTAAGTGTCTGTACTTACTTCAAGAGAGATCAGGAGAC	388
QY	591	ctccgcagatcatcctccctcttctctgctgctgaactgcgaactgctgtccttccctcgtcgt	650
Db	387	GCCCCCTTCGAGGTTCTTAACCTGTTCTGTCGGCGCTGACATTACGCGTCTGTTCTCTA	328
QY	651	tcttctcactacgctccggttctctctgttgtttaaacygggcagaaagaactcctgtatatat	710
Db	327	TCTTTCATCATTTCTGTGTTCTGTGTGCCAATATGGCTCAGGAAGATGTCCTCCCAACATAT	268
QY	711	tcaaacaccatttatatgagaccagttacaaactcattccaagaaggaagtgtctatagtctgc	770
Db	267	TCAACCAACCAATTAAAGAGGGCGTTAGAACGCTCAACAGGAAGATGCTTGTATGCTGCC	208
QY	771	gatttcagaagaagaagaagagatgysaa	802
Db	207	GATTTCAGAGAGAGAGAGAGAGAGGAGGA	176

RESULT	4
LOCUS	A1236084/c
DEFINITION	A1236084 687 bp mRNA EST 31-JAN-1999
ACCESSION	EST232646 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
VERSION	ROVDB21 3 end, mRNA sequence.
KEYWORDS	A1236084 A1236084.1 GI:3829590
SOURCE	ESF.
ORGANISM	Rattus sp.
	Rattus sp.
	Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
	Rattus.
REFERENCE	1 (bases 1 to 687)
AUTHORS	Lee,N.H., Glodok,A., Chandra,I., Mason,T.M., Quackenbush,J.,
TITLE	Kerlavage,A.N. and Adams,M.D.
JOURNAL	Rat Genome Project: Generation of a Rat EST (RESE) Catalog & Rat
COMMENT	Gene Index Unpublished (1998)
	Other ESTs: TC60155
	Contact: Lee, NH
	ATCC

RESULT	5		
AA946462/c			
LOCUS	AA946462	674 bp	mRNA
DEFINITION	EST201961 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone	EST	25-JAN-1999
ACCESSION	ROVAR42.3	end, mRNA sequence.	
VERSION	AA946462		
KEYWORDS	AA946462.1	GI:3106378	
SOURCE	EST.		
ORGANISM	Rattus sp.		
	Rattus sp.		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;		
	Rattus.		

REFERENCE	1 (bases 1 to 674)
AUTHORS	Lee,N.H., Glodet,A., Chandra,I., Mason,T.M., Quackenbush,J., Kerlavage,A.R. and Adams,M.D.
TITLE	Rat Genome Project: Generation of a Rat EST (RST) Catalog & Rat Gene Index
JOURNAL	Unpublished (1998)
COMMENT	Contact: Lee, NH ATCC
FEATURES	The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, USA Tel: (301)-838-3529 Fax: (301)-838-0208 Email: nhlee@igr.org Seq primer: M13-21. Location/Qualifiers 1..674
BASE COUNT	145 a 182 c 179 g 168 t
ORIGIN	/organism="Rattus sp." /db_xref="ATCC (inhost):201990" /db_xref="taxon:10118" /clone="ROVAR42" /clone_id="Normalized rat ovary, Bento Soares" /note="Organ: ovary; Vector: pUT33pac; Site_1: EcoRI; Site_2: NotI"
Query Match	27.6%; Score 231; DB 7; Length 674;
Best Local Similarity	68.1%; Pred. No. 2.7e-57;
Matches 337; Conservative	0; Mismatches 155; Indels 3; Gaps 1;
QY	311 ggggttcacgtgctggggagagatgcagatgltgtgaacagatgttaacaaggtca 370
Db	670 GGATTCACACTGCTTGGGGCCAAAGTGTACACAGTGTAAAGAAAGACTGCAGCGGCCAG 611
QY	371 gaactgcacaaaaaaggtgtgttaagactgttgccttggagacatlaacgatcaagaacg- 429
Db	610 GAACATACGGAGACAGGAGTGTAAAAACTGTGGCTTGGGAACTTTAAATGACCAAGAACGGC 551
QY	430 --ttggcatctgtcgagcccttgagacaactgtctcttggatgtagaagctgtgtgttgat 487
Db	550 GCCGCGTCTGCCGACCCCTGGACGACACTGTCTGTAGACGGAAGGTCTGTGCTTAAGAAAT 491
QY	488 gggagcaagagagagagacgtgtgtctgtgtgacccatctccagctgacctctctccggagga 547
Db	490 GGGACCAAGAGAAAGACGTGTGTGTGAGACCCCTGTGTGTAGGCTCTCTCCACAGTAC 431
QY	548 tccctgtgaccccgctgccttcgcgtgcagagagacgaacactctccgcagatcatctcc 607
Db	430 ACTCTACTGTGCTGTACTACTCCAGAGAGAAATCAGAGACGACGCCCTTGAGAGTCTT 371
QY	608 tctctctgtgacgtgcagctgcagctgtgtctctccgtgttcttctcagctcgt 667
Db	370 ACCTTGTCTCTGCGCCCTGACATTTAGCGCTGCTCTCTGTTCTTCTATCTTCTCTGG 311
QY	668 tctctgtgtttaaocggggcagaaagaactcctgtatatacttaaaacacattatg 727
Db	310 TTCTCTGTGCCCAATATGGCTCAGGAAGATTTCCCCCAATATTCAGAACCAATTAAAG 251
QY	728 agaccagtaacaactcactcaagaagagaatgtgtgttagctgcgattccagaagaaga 787
Db	230 AAGGGGTTAGAACTCACAAGAGAAAGATGCTGTACTGCGCGTTTCCAGAGAGAA 191
QY	788 gaagagagatgtgaa 802
Db	190 CAGAGAGAGAGAGGA 176
RESULT	6
LOCUS	AA087107 589 bp mRNA EST 23-OCT-1996
DEFINITION	mol3g01.1 Life Tech mouse embryo 10 5dpc 10665016 Mus musculus cDNA clone IMAGE:553488 5' similar to gb:J04492 Mouse T-cell

	receptor 4-1BB protein mRNA, complete cds (MOUSE);	mRNA sequence.
ACCESSION	AA087107	
VERSION	AA087107.1	GI:1630565
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
	1 (bases 1 to 589)	
	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,	
	Schellanderberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,	
	Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and	
	Waterston,R.	
TITLE	The WashU-HHMI Mouse EST Project	
JOURNAL	Unpublished (1996)	
COMMENT	Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lln.gov) for further information. MGI:334280 Seq primer: -28MJ3 rev1 from Amersham High quality sequence stop: 377. Location/Qualifiers 1..589 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="IMAGE:553488" /clone_1lb="Life Tech mouse embryo 10 5dpc 10665016" /tissue_type="embryo" /dev_stage="10.5dpc embryos" /lab_host="DH10B" /note="Organ: whole embryo; Vector: PCMV-SPORT2; Site_1: Salt: site_2: NotI; Cloned unidirectionally. Primer: Oligo df. 10.5dpc embryos. PCMV-SPORT2 vector."	
BASE COUNT	133 a 138 c 171 g 147 t	
ORIGIN		
Query Match	24.2%; Score 203.2; DB 1; Length 589;	
Best Local Similarity	67.6%; Pred. No. 4.1e-49;	
Matches 345; Conservative	0; Mismatches 158; Indels 7; Gaps 4.	
Db	13 tagatcatactgctgcagcatttcatacttgtagaaacagctgttacaatatagtagccac	72
	56 TGGTGTCCGTCATCATGTGCATTCTTGCCATGGGAAACAACACTTTACACAGTGTGTCTAT	115
Dy	73 tcgttgtcgtgctccaactttgagaagacaagaatcatcttgcaagatccttgaagttaacty	132
Dz	116 TGTCGTGCGTAGTGGCGCTGTGAAGAAGTGAGGCCGTCAGAACTCCTGTGATTAACGTG	175
Oy	133 ccacagctgtaaatctctgtgataataaacaggatcatttcagtlccctgctcccaaa	192
Pb	176 TCAGCCTGGTACTTTCTCGCAAAAATAC--AATCCAGTCTCAAGAGCTGCCCTCCCAAG	232
Qy	193 tagttctccacagcgagtgagacaagaagcctgttacatatcacagcgagtgaaagtgct	252
Rb	223 TACCTCTTCACACATAGGTGGAGACACCAGAACCTGTAACTCTCACAGAGTGTGTGACAGCTA	292
Oy	253 ttccagaccagaaagagtgcttctccacacccagaatgcagagtgltgactgacctccag	312
Dz	293 TTTCAGGTTCAGAGAGTTTTCCTCTTACCCACAACGCGGAGTGTGATTCATTTGAAGG	352
Oy	313 gtctacgtccctgggggcaagatgtgatcatgtgtataacagagattgtataaagaagtcacga	372
Dz	353 ATTCCATTGCTTGGGGCCACACTGTACACAGATGTGAAGAGACTGTCAGGCTTGACACAGA	412

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OY 373 a-cgcagcaaaaaaggtgtgtatgaagactgtgtcttgaggacattcaagatacaagacg-- 429
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 413 AGCTACGAGAACGAGGCTGTGCAAAACCTGTACCTGGGAACTTTAAATGACCAAGACGGGA 472
OY 430 tggatctgtgacccttgagcaaaactgtctcttgatggaagtcgtgtgcttggaaatgg 489
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 473 GGTGTCTGTGACCTTGCGGAGGAGTGGCTCTATTCTTATGATGTGTGC-TAAGACCGG 531
OY 490 gacgaagagagagagcgtgtgtctgtgagc 519
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 532 GACCACGAGAGAGACGCTGTGTGAGAC 561

RESULT 7
LOCUS A1664286 491 bp mRNA EST 10-MAY-1999
DEFINITION ue83h05.r1 Soares.NMPu Mus musculus cDNA IMAGE:149753 5',
similar to gb:J04492 Mouse T-cell receptor 4-1BB protein mRNA,
complete cds (MOUSE);, mRNA sequence.
ACCESSION A1664286
VERSION A1664286
KEYWORDS EST.
SOURCE A1664286.1 GI:4767869
ORGANISM house mouse.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 491)
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:935357
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 419.
FEATURES
source location/Qualifiers
1..491
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:149753"
/clone_1id="Soares_NMPu"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: uterus; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; 1st strand cDNA was prepared from
pregnant mouse uterus, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."
BASE COUNT 114 a 118 c 135 g 124 t
ORIGIN

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Db 161 TCAGCTGTAATCTTCTCAGAAAATAC---AATCAGCTGCAAGACGCTGCCCAAG 217
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 193 tagttctccagcgaggtgtgacaagaagcctgtgacatgcaagcagctgtgaaagtgct 252
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 218 TACCTTCTCCAGCATATGATGGACACCAACTGATACATCTGCAGAGTGTGCGAGCTA 277
OY 253 ttccagaccaggaagagtgcttccaccagcaatgcagagtgtagctcaactccagg 312
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 278 TTTCAGGTTCAAGAGGTTTGTCTCTACCCACAGACGCGAGTGTGATGATGGAAGG 337
OY 313 gttcaactgcttgaggcgagatgcagcatgtgtgaacagagattgtaaacagtgcaaga 372
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 338 ATTCATTGCTTGGGGCCACAGTGCACCATGTGAAGAGACTGCAGGCTGGCCAGA 397
OY 373 actgcaaaaaaggtgtgaagactgtgtcttgaggacattcaagatcagaagacg--- 429
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 398 GCTACGAGAGCGAGGTTCCAAAACCTGTAGCTGGGAACATTTAAATGACCAAGACGATAC 457
OY 430 tggcatctgcgacccttgacaactgtctt 462
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 458 TGGCCTGTGTGACCTTGACGACGACTGCTCTCT 490

RESULT 8
LOCUS A1172529/c 332 bp mRNA EST 05-JUL-1999
DEFINITION UI-R-C2p-nu-g-01-0-UI.s1 UI-R-C2p Rattus norvegicus cDNA clone
UI-R-C2p-nu-g-01-0-UI 3', mRNA sequence.
ACCESSION A1172529
VERSION A1172529.1 GI:3712569
KEYWORDS EST.
SOURCE A1172529.1 GI:3712569
ORGANISM Norway rat.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 332)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704447
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msouares@blue.weeg.uiowa.edu
The sequence tag present in the cDNA between the NotI site and the
oligo-dr track served to identify it as a clone from the normalized
adult ovary library. cDNA library preparation: M. Fatima Bonaldo,
Ph.D. Clone distribution: clones will be available through Research
Genetics This clone is also available through the I.M.A.G.E.
Consortium at LNL (info@image.lnl.gov). IMAGE ID=178664 The
following repetitive elements were found in this cDNA sequence:
1-37, >AT_rich#low_complexity
Seq primer: M13 Forward
POLYA-No.
FEATURES
source location/Qualifiers
1..332
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C2p-nu-g-01-0-UI"
/clone_1id="UI-R-C2p"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C2p
library is a subtracted library derived from the UI-R-C1
library, which is a subtracted library derived from the

```


library, which is a subcloned library derived from UI-R-C0 library. The UI-R-C0 library consisted of a

```
source 1. .688
        /organism="Homo sapiens"
        /db_xref="GDB:5182340"
        /db_xref="taxon:9606"
```

```
/db_xref="taxon:9606"  
/clone="IMAGE:1118659"  
/clone_lib="NCI_CGAP_Lu1"  
/tissue_type="lung tumor"
```

```

/organism="Homo sapiens"
/db_xref="GDB:1246259"
/db_xref="taxon:9606"
/clone_image="301335"
/clone_lib="Soares fetal_lung_NbHL9w"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: lung; Vector: p773D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - Oligo(dT) primer"

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Email: genome-res@tc.riken.go.jp,
URL: <http://genome.irc.riken.go.jp/>
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